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/lab_hogt="DH10B TonA"
/clone lib="NHH MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all:*Moi; Site_2: BamH; Oligo-dT primed using primer
all:*Moi; Site_2: BamH; Oligo-dT primed using primer
site_2: A bamd normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, Wational Institutes of Health). Note: This is
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ANNCATGTGGTGGCCANNCCAACAGGAAGCAAGAAACCATAAGGGGAGAAAAGCCCCGC 746
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Search completed: January 31, 2004, 15:28:25 Job time : 1681.59 secs

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30344820"
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/db_xref="taxon:9606"

/dlone="ILTAGE:5596303"

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/dlone lib="NH1MGC 125"

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                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12364 row: o column: 16
High quality sequence stop: 535.
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     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Array Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: NDAM381 row: 1 column: 13
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--ArgAlaGlu 171
                                                                             596 recegecececerecirearecearanececaecitraceseraness
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
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ACCONCORT_6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503

BM906521
preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH MGC library."

a 243 c 260 g 133 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1230)
                                                                                                                                                                                                                                                            GGCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCCCCCCTGGGGCCACCCAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 lSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGlu-AsnV
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                                                                                                                                                                                                                                                                                                                                                                                                              212 CGCTCGGCTCTCTGGGGTGTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 1AlaValValGlyGluGlnPheThrLeuGluCygGlyProProTrpGlyHisProGluPr
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190
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8
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                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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918.50
91.47$
90.05$
62.27$
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Best Local Similarity:
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DEFINITION
                                               BASE COUNT
ORIGIN
                                                                                                                Pred. No.:
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AGENCOURT 13761727 NIH MGC 147 Homo sapiens cDNA clone IMAGE:30343790 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Jr. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM379 row: a column: 15
High quality sequence stop: 475.
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                                362
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 TGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 797)
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//clone lib="NIH MGC 147"
//note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-Khol; Site_2: BanH; Oligo-dT primed using primer
all-Khol; Site_2: BanH; Oligo-dT primed using primer
all-Khol; Site_2: BanH; Oligo-dT primed using primer
insert size_2: 3. kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
                                                                                                                                                                                 CTGGCTGTGCGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGC
                                                                                                                                                                SerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/db_xref="taxon:9606"
/clone="IMAGE:30343790"
/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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CB961002.1 GI:30217119
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Homo sapiens
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VERSION
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AUTHORS
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CB961002
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160

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                                                                                                                                        BM914311.1 GI:19364690
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Pred. No.:
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KEYWORDS
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM360 row: n column: 04
High quality sequence stop: 535.
Location/Qualifiers
                                                                                                                                                                                                                                                                                      803
194
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1
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Matches:
Conservative:
Mismatches:
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1002.50
94.84$
91.08$
67.97$
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Best Local Similarity:
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BM914311
AGENCOURT 6615385 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5479976
5, mRNA Sequence.
BM914311
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: b column: 09
High quality sequence stop: 535.
91 AsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGlu 110
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Conservative:
Mismatches:
Indels:
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                                                     --- GluProGlnAspTyrThrGluProValGlu
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493 140 553

373 100 433 120

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733 216 233

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mRNA linear EST 01-MAY-2003
Homo sapiens cDNA clone
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                               141 ThrvalSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHis--ThrV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ysvalAlaThrAsnSerAlaGlyHisArg---GluSerArgAlaAlaArgValSerIleG 199
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                                                 AlavalvalGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro
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                                                                                            LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr
                                                                                                                                                                          AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly
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                    41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
                                                                                                                                                                                                                 374 GACCTGGGTGTCTACACATGTGAGGCCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC
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1 (bases 1 to 803)
1 (NIH-WGC http://mgc.nci.nih.gov/.
National Intp:/tutes of Health, Mammalian Gene Collection (MGC)
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/dsv stage="adult, 36 yr"
/lab_host="adult, 36 yr"
/lab_host="nH108"
/clone lib="tupsk; dorsal root ganglion"
/clone lib="tupsk; dorsal root ganglion"
/note="vector: pcW^-SPORT6 (Life Technologies); Site_1:
Not!, Site_2: Sall; Cond using the following adaptors:
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTACTTCAGATCCCAGCGCCCCCT(15)-3', Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
Technologies."
                                                                                                    BUBBO126
AGENCOURT 7982449 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6186214 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CONG Sequencing by: Agencourt Bioscience Corporation
CONG Gistribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11578 row: d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
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nGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGlu 218
                  610 GGAGCCCCAGGACTACACGGAGCCTGTGGACTTCTGGCTGTGCCGAATCAGCTGGAC 727
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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/flome_lib="WHW MGC 116"

/pote="Crgan: pooled colon, kidney, stomach; Vector:
potWY-SpotExfs: Site_1: Not!; Site_2: EcoRV (destroyed); RNA
gource anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
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/organism="Homo sapiens"
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                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5188652"
/lab_host="DH10B"
 High quality sequence stop: 723
Location/Qualifiers
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603048384F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188652 5',
mRNA sequence.
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                     418 GCTAGGCTGTCTGTGGCTGTCCTCCAGGAGGACTTCCAGATCCAACCTCGGGGACACGTG
                                                                                                                                                                                                                                                                       201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArglleGlnLeuGluAsnVal
                                                                                                                  81 AspleuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly
                                                                                                                                     358 ATCCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTGGGGCACAGCAGCAGTGAGCCGGGGT
                                                                                                                                                                                      AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11471 row: g column: 21
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Goroto Fall-length cDNAs

I Sachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamara,M., Nishi,K., Nomura,K., Numazaki,A., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sano,H., Saaaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Mateumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yonda, Y., Mintanata, M., Inoue, Y., Kira, A., and Hayanizaki, Y., Rikki integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409 (6821), 685-690 (2001)
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                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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VGESLVIECGPPWGYPKPSVSWWKDGKPLVLOPGRRTVSGDSIMVSRAEKNDSGTYMC
ANNINAGORESRAARVS10ESQDHKEHLELLAVRTOLENDYLLINPEPYKGPKEPSVW
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ILSWPPRSPGVPLLIGTSTRYPGSSPPVRSSPPVRSSPRYPAARRFPSKLAGTSSPWA
SSDSLCSRRGLCSPRMSLTPTEAWKAKKQELHQANSSPLLRGSHPMEIWAWELGSRA
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PQSQCVEKLQAPSSDPLPAAPLSVLNSSRPSSPQASFLSCPSPSSSNLSSSSLSSLEE
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ADTHFGSCPGQWLWIALASVWIPGRLTVSSLMPHHLPPLGVISP"
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama KIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Eax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
4. 3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; putative
similar to MAGIC ROUNDABOUT [Homo sapiens] (SPTR|AAL31867,
evidence: FASTY, 77.6%ID, 99.5%length, match=3012)"
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/db_xref="RANOM DB:E030049D17"
/db xref="taxon:10090"
/clone="E030049D17"
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/db_xref="G1:26352440"
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COMMENT

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Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030049D17 product:similar to MAGIC ROUNDABOUT [Homo AR087555]
                                                                                                                                                                                                                                                                      101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GCTAGGCTGTCTGTGGCTGTCCTCCAGGAGACTTCCAGATCCAACCTCGGGACACAGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AlavalValGluGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
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             243
                                                                                                             US-10-047-021-86_COPY_28_303 (1-276) x AK004723 (1-3689)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
          74.73% 72.03% 11
             Similarity:
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Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, T., Toyan, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of Direct Submission

L. Submitted (10-07u-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, Rax:81-45-503-9216)

On Dec 10, 2002 this sequence version replaced gi:12836108.

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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TSSPWASSDSLCSRRGLCSPRWSLTPTEAWKAKKKQELHQANSSPLLRGSHPMEIWAW
ELGSRASKNLSQSPGEAPRAVVSWRAVGPQLHRNSSELASRPLPPTLSLRGASSHDP
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BODSVLTPEEVALCILELSADGEETPTNSVSPMPRAPSPPTVGYIS IPTCSGLADMGR
AGGGVGSEVGNLLYPPRPROFTPTPSEGSLANGWGSASEDNVPSAASLVSSSOGSFLA
DTHFARALAVAVDSFGLSLDPREADCVFTDASSPPSPRGDLSLTRSFSLPLWEWRPDM
                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; putative
similar to MAGIC ROUNDABOUT [Homo sapiens] (SPTR|AAL31867,
evidence: FASTY, 77.6%ID, 99.5%length, match=3012)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon start=1
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/db_xref="MG1:1921394"
/translation="MGQGEEPRAAMGSGGTGLLGTEWPLPLLLLFIMGGBALDSPPQI
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Matches:
Conservative:
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/strain="C57BL/6J"
/db_xref="FANTOM DB:1200012D01"
/db_xref="MG1:1907253"
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/organism="Mus musculus"
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clone="1200012D01"
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100 420

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Percent Similarity:

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                                                        3.48e-74
1081.50
79.78%
79.04%
73.32%
                                                                                                                Percent Similarity:
Best Local Similarity:
                            Alignment Scores:
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AK004723 3689 bp mRNA linear HTC 05-DEC-2002 Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012201 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

AK004723 LOCUS DEFINITION

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Li Nature 420, 563-573 (2002)

E (bases 1 to 3689)

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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Ano, H., Arakawa, T., Bono, H., Garninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Konon, H., Kouda, M., Kasukawa, T., Kato, H., Kayai, J., Kojima, Y., Konno, H., Kouda, M., Kowai, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,Y., Izawa,M., Ohara,E., Watahiki,M., Rikk integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409 (6821), 685-690 (2001)
                                                                                                                                                             Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
AK004723.2 GI:26334429
HTC; CAP trapper.
Mus musculus (house mouse)
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/tissue_type="pre-eclamptic placenta"
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/lab.host="blands TonA"
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/clone lib-"NIH NIH MGC 148"
/clone lib-"NIH MGC 148"
/clone lib-"
/clo
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: c column: 24
High quality sequence stop: 637.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 13622686 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30337143 5', mRNA sequence.
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM361 row: 1 column: 16
High quality sequence stop: 578.
161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/organism="Homo sapiens"
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/clone lib="Homo sapiens PETAL BRAIN"
/clone lib="Homo sapiens PETAL BRAIN"
/note="Corgan: brain; Vector: pCMVSBORT_6; lst strand cDNA was primed with a NotI-oligo dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6
GGGAAACCCTGGCCCTCCAGCCCGGAAGGCACACACAGTGTCCGGGGGGGTCCCTGCTGATG 495
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cgi-bin/cluster.cgi?seq=CSODF001BE12QP1&cluster=6206.r. Contact
Feng Liang Email : fliang@lifetech.com WIR. :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSODF001BE12QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                        Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. This sequence belongs to sequence cluster 6206.r
more information about this cluster, see
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/db_xref="taxon:9606"
/clone="CSODF001Y124"
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BM921911 1006908 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753515 5', mRNA sequence.

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/lab host="DH10B"
/clone lib="NIH MGC lis"
/clone lib="NIH MGC lis"
/clone lib="NIH MGC lis"
/note="Grgan: pooled brain, lung, testis; Vector:
pCWV-SPORTE; Site li Not; Site 2: EccRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; l
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
4 others
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                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1019)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                        Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clond clistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate:/LLAM12789 row: g column: 20
High quality sequence stop: 697.
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Matches:
Conservative:
Mismatches:
Indels:
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                                               Homo sapiens (human)
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On Feb 15, 2001 this sequence version replaced gi:12893123.

On Feb 15, 2001 this sequence version replaced gi:12893123.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSODIO75CH07QP1&cluster=6206.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO75CH07QP1.
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primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."
348 c 369 g 212 t 36 others
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11 (bases 1 to 1201)
11,4.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
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AUTHORS
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                              Direct Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/Linn. at: http://image.llnl.gov
Series: IRAK Plate: 84 Row: i Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction
This clone has the following problem: frame shifted.
Location/Qualifiers
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                                                                                                                                                                      WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Anup Madan, Assica Fahey, Erin Helton, Mark Netteman, Anurad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="Ovary, pooled from 3 adults"
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/lab host="DH10B"
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1232 c 1046 g 708 t
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AUTHORS
TITLE
JOURNAL
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29: gb_gss2:*

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BC039602
Homo sapiens, Similar to roundabout homolog 4, magic roundabout
(Drosophila), clone IMAGE:5590503, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3758)
           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                          SUMMARIES
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CB961002
BM906521
CB959649
BG745318
CB961529
CB961529
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A1116483
BY704924
AA577940
BX475177
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BX475172
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CB993951
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BB871780
BY285423
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CB997292
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BB664621
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CA394658
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CB994099
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AK004723
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Homo sapiens
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10013.5
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                        Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CGD2 1/USPTO spool p/USIO407021/runat 30012004 145453 24574/app query.fasta_1.910
-DB=EST -QEMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b1000m62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b1000m62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=D100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNGM=EXT -NORM=EXT -HEAPSIZE=550 -MINLEN=0 -MAXLEN=200000000
-USER=USIO047021 @CGN 1 1 4399 @runat 3012004 145453 24574 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                           (without alignments)
4005.776 Million cell updates/sec
                                                                                          January 31, 2004, 12:28:30 ; Search time 1674.59 Seconds
                                                                                                                                                     US-10-047-021-86_COPY_28_303
1475
1 QDSPPQILVHPQDQLFQGPG.....SGPRLPREARELRGQRRNTG
                                                                                                                                                                                                                                                                                                                                             45562784
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                           - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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em_gss_inv:*
em_gss_pln:*
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seq length: 200000000
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gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
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Maximum DB
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BQ890126 AGENCOURT CB997292 AGENCOURT CB961002 AGENCOURT CB961002 AGENCOURT BM906521 AGENCOURT CB959649 AGENCOURT CB951529 AGENCOURT CB961529 AGENCOURT CB961529 AGENCOURT CB961529 AGENCOURT CB961524 AGENCOURT AL602474 DKFZE6860

BX418142 BX418142 CB994099 AGENCOURT CB996189 AGENCOURT AK004723 Mus muscu

Mus muscu 603048384

AK087355 BI762862

BC039602 Homo sapi AL553360 AL553360 BM921911 AGENCOURT BE233526 139756 MA BY727209 BY727209 BX474842 DKFZp686M BB664621 BB664621

BX475138 DKFZp6860 CA394658 cs54c07.y BE376779 601227331

BX474746 DKFZp686B Bx520802 RZpD Mus AII16483 ud74c06.y BY704924 BY704924

AA577940 n120d01.8 BX475177 DKFZp686F AL039859 DKFZp434E BI159602 602920006 BX475172 DKFZp686E

Bx492967 Homo sapi BB839755 BB839755 CB993951 AGENCOURT BIB36220 603085778 BB871780 BB871780

AMGNNUC:N UI-M-FY0-

CB585643 CB527493

BY270114 BY270114 CB527120 UI-M-FY0

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB e Maximum DB e

Database

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Q9gpp6 drosophila
Q9vp27 drosophila
Q9vp27 drosophila
Q9vp27 drosophila
Q9dq13 rattus norv
Q9qq13 rattus norv
Q9qvn5 rattus norv
Q9vp7526 homo sapien
Q9vp75 rattus norv
Q9fr14 homo sapien
Q9fr16 rattus norv
Q9fr17 homo sapien
Q9fr18 rattus norv
Q9fr18 rattus norv
Q9fr18 rattus norv
Q9fr18 rattus norv
Q9fr18 drosophila
Q9v24 drosophila
Q9v24 drosophila
Q9c24 drosophila
Q9c44 gallus gall
Q8cbrf mus musculu
Q8cbrf mus musculu
Q8cbd3 mus musculu
0988w4 brachydanio
                                                Q8bj59 mus musculu
              Q9w213 drosophila
O44924 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20530916; Pubmed=11076864;
Huminiecki L., Bicknell R.;
IIn silico cloning of novel endothelial-specific genes.";
Genome Res. 10:1796-1806(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMO066; FN3; 2.
SMART; SM00408; IGG2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain.
SEQUENCE 1007 AA; 107457 MW; E43F246C59BE1415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huminiecki L., Bicknell R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF361473; AAL31867.1; -.
Genew; HGNC:17985; ROBG.
InterPro; IPR003961; FN III.
InterPro; IPR003101; Ig-like.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00041; En3; 2.
Pfam; PF00047; ig; 2.
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Last annotation update)
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                                                                                              001632
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Q961K8
Q9VZZ4
P97528
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Q8BRT6
Q8CBD3
Q90924
Q42414
Q62845
Q8C6X1
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                                              Q8BJ59
Q9GPP6
Q9VPZ7
                Q9W213
O44924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
27.2
26.8
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226.7
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224.0
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23.5
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28WZ75
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Q8uvd7 xenopus lae
Q90270 brachydanio
Q92214 mus musculu
Q9hck4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8wz75 homo sapien
Q96jv6 homo sapien
Q8c310 mus musculu
Q8teg1 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8teg1 homo sapien
Q96ms0 homo sapien
O55005 rattus norv
Q9y6n7 homo sapien
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Q90z42 gallus gall
Q8uvd7 xenopus lae
                                                                                                                January 30, 2004, 15:51:24 ; Search time 29.0777 Seconds (without alignments) 2449.385 Million cell updates/sec
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                                                                                                                                                                                  US-10-047-021-86_COPY_28_303
1475
1 QDSPPQILVHPQDQLFQGPG......SGPRLPREARELRGQRRNTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
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Q96JV6
Q8C310
Q8TEG1
Q96MS0
O55005
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090242
08UVD7
090270
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL 23:*

1: sp_archea.*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*
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sp_bacteriap:*
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sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Match
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69.8
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Gaps

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88.9%; Score 1311; DB 4; Length 1007; 98.8%; Pred. No. 1e-104; cive 1; Mismatches 2; Indels 0

Query Match
Best Local Similarity 98.8
Matches 243; Conservative

Q90241 gallus gall Q90269 brachydanio Q988w3 brachydanio

Q90241 Q90269 Q98SW3

13

1303 1029.5 748

Result No.

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159 AVVGESLVLECGPPWGYPKPSVSWWKDGKPLVLQPGRRTVSGDSLMVSRAEKNDSGTYMC 218
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181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LLLQPPARGHAHDGQ-ALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AVVGEQPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                        208 VAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSPPOILVHPQDOLLOGSGPAKMRCRSSGQPPPTIRWLLNGQPLSMATPDLHYLLPDGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK087355; BAC39850.1; -.
SEQUENCE 1016 AA; 108461 MW; DE70683C63AECD8E CRC64;
                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to MAGIC ROUNDABOUT.
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Last annotation update)
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                                                                                                                                                                                                                                                                                              1016 AA.
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Matches 193; Conservative
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SEQUENCE FROM N.A.
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                                                                                                     241 WKVSGP
                                                                                                                                                          WKVSGP
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Q8C310;
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                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                             VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRAVWLX 240
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                                                       QDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                     28 QDSPPQILVHPQDQLFQGPGFARMSCQASGQPPPTIRWLLNGQPLSWVPPDPHHLLPDGT
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P. SEQUENCE FOAT.

A ISSUE-Placente;

A Nishikawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugana T., Otsuki T., Takabashi-Fuji A., Hara H.,

A Arita M., Nabekura T., Toghia S., Kawai Y., Saito K., Yamamoto J.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Arita M., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

R. Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AKO27852; BABS5411.1;

BR InterPro; IPR003961; FN III.

BR InterPro; IPR003961; FN III.

BR InterPro; IPR003961; Ig_MHC.

BR Fâmi; PF000041; fn3; 2.

BR Fâmi; PF000041; fn3; 2.

BR SMART; SM00060; IGC2; 1.

BR SMART; SM00408; IGC2; 1.

BR SMART; SM00408; IGC2; 1.

BR HYDOTHELical protein; Immunoglobulin domain.

SEQUENCE 792 AA; 85419 WW; PC6DC05275B7B234 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14946.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo.
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118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
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HSSP; P56276; ITLK.
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                                                                     Matches 109; Conservative
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Local Sir.
92;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ31982.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NEDO human cDNA sequencing project.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKOS6544; BAB71212.1;
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR003961; Ig_c2.
InterPro; IPR003069; Ig_c2.
InterPro; IPR003069; Ig_c2.
InterPro; IPR003069; Ig_mHC.
Pfam; PP00041; fn3; 3.
Fam; PR004047; fg; 5.
FNART; SM00406; IGc2; 5.
FR00301TE; PSS0835; IG_LIKE; 5.
FROMSTE; PSS0835; IG_LIKE; 5.
                                                                                                                            EMBL, AKO7416; BAB84989.1; -

REMBL, AKO7416; BAB84989.1; -

RIDEAPRO; IPR0013961; FN III.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

RIDEAPRO; IPR003598; Ig-C2.

RIDEAPRO; IPR003006; Ig-MHC.

REMBL; PR000041; fn3; 2.

REMBL; SMO0409; IG3; 1.

REMART; SMO0060; FN3; 2.

REMART; SMO0060; FN3; 2.

REMSRT; SMO0108; IG-LIKE; 1.

REMONITER PS0835; IG-LIKE; 1.

REMONITER PROSITE: PS0835; IG-LIKE; 1.
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96.5%; Pred. No. 3e-56;
ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702 AA; 75340 MW; D668FBE4BCAFDCC6 CRC64;
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Best Local Similarity 96.5
Matches 139; Conservative
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   TISSUE=Spleen;
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01-DD 01-D
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120 SGALFF---PRIVH---GRRARPDEGVYTCVARNYIGAAASRNASLEVAVLRDDFRQSPG 173
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                                                                                                                                                                                                                                                                                                                                                                                  60 EDAMPRIVEQPPDLLVSRGEPATLPCRAEGRPRPNIEWYKNGARVATVREDPRAHRLLLP
                                                                                                                                                                                                                                                                                                1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDP--HH-LLLP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Roundabout controls axon crossing of the CNS midline and defines a novel subfamily of evolutionarily conserved guidance receptors."; Cell 92:205-215(1998).
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TISSUE-Spinal cord;
MEDLINE-Spi117249; Pubmed=9458045;
Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
Goodman C.S., Tear G.;
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30.4%; Score 448.5; DB 4; Length 1034; 43.1%; Pred. No. 3.8e-30; ive 23; Mismatches 90; Indels 31;
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R InterPro; IPR003598; Ig_c2.

R InterPro; IPR003598; Ig_c2.

R InterPro; IPR003066; Ig_MHC.

R PEam; PF00041; En3; 3.

R SWART; SM00064; FN3; 3.

R SWART; SM00408; IGc2; 5.

R PR051TE; PS50385; IG_LIKE; 5.

R Immunoglobulin domain; Receptor.

SEQUENCE 1651 AA; 180747 MW; FA2452DD46E186B7 CRC64;
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01-UNN-1998 (TrEMBLrel. 06, Last sequence update)
01-UNAR-2003 (TrEMBLrel. 23, Last annotation update)
Transmembrane receptor Robol.
Rattus norvegicus (Rat).
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85 SGSLFFLR-----IVHGRKSRPDEGVYICVARNYLGEAVSHNASLEVAILRDDFRQNPS 138
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                                                                                                                                Wu M.C., Lowe N., Fordham R., Rabbitts P.;
"The mouse homologue of human DUTI/H-robol gene: protein sequence and chromosomal location.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y17793; CAAA76850.1; -.
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vargesson N., Luria V., Messina I., Erskine L., Laufer B.; "Expression patterns of Slit and Robo family members during vertebrate limb development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.2%; Score 445.5; DB 11; Length 1612; Best Local Similarity 41.7%; Pred. No. 1.2e-29; Matches 91; Conservative 31; Mismatches 87; Indels 9;
                                                                                                                                                                                                                                                 MGD, MGII1274781 Robol.

R InterPro; IPR00110; Ig_like.

R InterPro; IPR00110; Ig_like.

R InterPro; IPR00110; Ig_like.

R InterPro; IPR001596; Ig_WHC.

R Pfam; PP00041; fin3; 3.

R SMART; SM0066; FN3; 3.

R SMART; SM00466; IG; 5.

R PROSITE; PS50835; IG_LIKE; 5.

R PROSITE; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=21366016; Pubmed=11472852;
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BMBL, AF364047, AAK44293.1; -.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 3.
SWART; SM00408; IGc2; 3.
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                                                                                                  SEQUENCE FROM N.A.
                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ODSPPOILVHPODOLFOGPARMSCRASGOPPFTIRWLLNGOPLSMVPPDPHH---LLP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M., Goodman C.S., Tear G.; Rewndabout controls axon crossing of the CNS midline and defines novel subfamily of evolutionarily conserved guidance receptors."; Cell 92:205-215(1998).
                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.3%; Score 446.5; DB 4; Length 41.7%; Pred. No. 1e-29; ive 31; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 5.
SEQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;
                                                                                  238 YVCVGTIMMVGERESKVADVTVLERPSFVKRPSNLAVTV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                PRT; 1651 AA
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                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98117249; PubMed=9458045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew, HGNC:101249; ROBO1.
InterPro; IPR003961; FN III.
InterPro; IPR003061; Ig—like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003066; Ig_V.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF040990; AAC39575.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         089026;
01-NOV-1998 (TrEMBLrel. 08, C.
01-NOV-1998 (TrEMBLrel. 08, L.
01-MAR-2003 (TrEMBLrel. 23, L.
Duttl protein.
ROBOI OR DUTII.
                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91; Conservative
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                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                             Roundabout 1.
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109Y6
109Y6
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109Y6
101-N

Matches

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RESULT 8 089026 ID 08902 AC 08902 DT 01-N DT 01-N DE DUEL: GN ROBO3

84

Gaps

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MEDLINE=21270059; PubMed=11376489;

MEDLINE=21270059; PubMed=11376489;

MEDLINE=21270059; PubMed=11376489;

MEDLINE=21270059; PubMed=11376489;

MEDLINE=21270059; PubMed=11376489;

MEDLINE=21270659; PubMed=11376489;

MEDLINE=216206010.";

MEDLINE=217606010.";

MEDLINE=2176060010.";

MEDLINE=217606000.";

MED
58 DGTLLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMCVATUSAGHRESRAARVSI-QEPQDYTEPV-----ELLAVRIQLENVTLLNPDPAE 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 EDSPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTVEMYKDGERVETDKDDPRSHRMLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,
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                                                                                                                                200 KYVCVGTNMVGERESEVAELTVLERPSFLRRPSNMAVTV 238
                                                                                            177 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
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36.4%; Pred. No. 1.6e-27;
iive 38; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1344 AA
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 GPKPRPAVWLXWK 242
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es 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain.
SEQUENCE 1513 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSLFFLR-----IVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEVAILRDDFRQNPS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 DGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
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                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                     1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID=8355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Connor R.M., Key B.;

Connor R.M., Key B.;

Tole for Roundabout-1 in neural differentiation and axon pathfinding in the Kenopus forebrain.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF461119; AL66361.1;

InterPro; IPR00351; FN III.

InterPro; IPR003508; Ig C2.

InterPro; IPR03598; Ig C2.

InterPro; IPR03006; Ig MHC.

Pfam; PP00041; fig. 5.

Pfam; PP00047; ig. 5.
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                                                                                                                                                                                  DB 13; Length 330;
                                                                                                                                                                                  Query Match 30.0%; Score 442.5; DB 13; Length Best Local Similarity 41.3%; Pred. No. 3.1e-30; Matches 90; Conservative 32; Mismatches 87; Indels
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                                                                                            330
36725 MW; 0613488F78CEBE61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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SMART; SM00408; IGC2; 5.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain.
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         PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 40.6
Matches 89; Conservative
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                                    Immunoglobulin domain.
NON_TER 1 1
NON_TER 330 330
SEQÜENCE 330 AA; 36
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85

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178 YMCVATNSAGHRESRAARVSI-QEPQDYTEPV-----ELLAVRIQLENVTLLNPDPAE 229
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Vargesson N., Luria V., Messina I., Erskine L., Laufer E.;
"Expression patterns of Slit and Robo family members during vertebrate
                                                                                                                                                                                                                                                                                                                                                                1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                               Length 1380;
                                                                                                                                                                                                                                                                               / Match 27.4%; Score 404.5; DB 4; Length Local Similarity 36.0%; Pred. No. 3.4e-26; nes 91; Conservative 36; Mismatches 95; Indels
                                                                                                                                                                                                                                                SEQUENCE 1380 AA; 151426 MW; 45EF63E2EFA26732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Roundabout2 protein (Fragment).
                                                                  InterPro; IPR003961; FN III.
InterPro; IPR003109; Ig-like.
InterPro; IPR003598; Ig-c2.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3.
SMART; SM00060; FN3; 3.
SMART; SM000608; IG-LIKE; 5.
PROSITE; PS50835; IG-LIKE; 5.
Hypothetical protein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 AA.
code for large proteins in vitro.";
DNA Res. 7:373-281(2000).
EMBL; AB046789; BAB13394.1; -.
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     limb development.";
Mech. Dev. 106:175-180(2001).
Mech. Dev. 106:175-180(2001).
InterPro; IPR007110; Ig-like.
InterPro; IPR003588; Ig-C2.
InterPro; IPR003066; Ig_HHC.
Pfam; PP00047; ig; 3.
SMART; SM0408; IGc2; 3.
Immunoglobulin domain.
NON_TER 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPKPRPAVWLXWK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 -- DPQPTV--RWK 261
                                                             Genew; HGNC:10250; ROBO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090Z41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090241
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 SGALFF---PRIVH---GRRSRPDEGVYTCVARNYLGAAASRNASLEVAVLRDDFRQSPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 YMCVASNMAGERESGAAELVVLERPSFLRRPI------NQVVLADAPVNFLCEVQG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ODSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDP--HH-LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMCVATNSAGHRESRAAR-VSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20450683; Pubmed=10997877;
Nagase T., Kivuno R., Nakayama M., Hirosawa M., Ohara O.;
Nagasel T., Kivuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIÀA1568.
Homo sapiene (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.1%; Score 414.5; DB 11; Length 39.9%; Pred. No. 4.5e-27; ive 27; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        1344 AA; 143439 MW; 8B0060341C49CFEA CRC64;
                                                                                                                                                                                Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF060570; AAD11628.1; -.
HSSP; P56276; ITLK.
            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein KIAA1568 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                             MGD; MGT:1343102; Rbig1.
InterPro; IPR003961; FN III.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003508; Ig_MHC.
Pfam; PP00041; fn3; 3.
Pfam; PP00041; fn3; 3.
SMART; SM00408; IG_C2; 5.
PROSITE; PS50835; IG_LIKE; 5.
            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAX-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPKPRPAVWLXWK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 DPQPN----LHWR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 39.9
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain. SEQUENCE 1344 AA; 14
                                                                                        Mus musculus (Mouse).
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                           Rig-1 protein.
RBIG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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RX MEDLINE=21270059; PubMed=11376489;
RT Lee J.S., RAY R., Chien C.B.,
RT "Cloning and expression of three zebrafish roundabout homologs suggest roles in axon guidance and cell migration.";
RT roles in axon guidance and cell migration.";
Dev. Dyn. 221.216-230(2001).
BR EMBL, AR31036; AAK584281.;
DR REPEO, PR0030954; FN III.
DR INTERPO, IPR0030951; FN III.
DR INTERPO, IPR0030961; FN III.
DR INTERPO, IPR0030961; Ig_-1ike.
DR INTERPO, IPR0030061; Ig_-1ike.
DR Fam; PF00041; fn3; 3.
DR Fam; PF00041; fn3; 3.
DR FAM; SM00060; FN3; 3.
DR SWART; SM00060; FN3; 3.
DR SWART; SM00060; FN3; 3.
DR SWART; SM00060; IG_LKE; 5.
KW Immunoglobulin domain; Repeat.
SEQUENCE 1389 AA; 151913 MW; E4268BE8839DD08F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                              9
                                                                                                                                                                     58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
                                                                                                                                                                                                                118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                        178 YMCVATNSAGHRESRAARVSI-QEPQDYTEPV-----ELLAVRIQLENVTLLNPDPAE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 DGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                            28 EDAAPRIVEHPSDLIVSKGEPATLNCKAEGRPTPMVEWYKDGERVETDREDPRSHRMLLP
                                                                                         1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 401.5; DB 13; Length 1389; 36.7%; Pred. No. 6.3e-26; ive 36; Mismatches 96; Indels 27;
                               DB 13; Length 333;
                                                         95; Indels
333 AA; 37689 MW; 47607C05AD84C7B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                          27.4%; Score 403.5; DB 1:
36.0%; Pred. No. 7.4e-27;
ative 36; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1389 AA
                                                                                                                                                                                                                                                                                                                                   230 GPKPRPAVWLXWK 242
                                                                                                                                                                                                                                                                                                                                                                249 -- DPQPTV--RWK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 36.78 Matches 92; Conservative
                                                         91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roundabout 3.
 SEQUENCE
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                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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GenCore version 5.1.6
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. OM protein - protein search, using sw model

January 30, 2004, 15:45:39 ; Search time 9.53368 Seconds (without alignments) 1361.423 Million cell updates/sec Run on:

US-10-047-021-86_COPY_28_303 1475 1 QDSPPQILVHPQDQLFQGPG.....SGPRLPREARELRGQRRNTG 276 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription		P22063 rattus norv	Q02246 homo sapien	-		P16621 drosophila	rattus		homo 88		homo 85		mus r	homo		mus r	drosop	P13590 gallus gall	001761 caenorhabdi	-	O15394 homo sapien	Q15746 homo sapien	นาย ก	80 8	P13594 mus musculu	_	homo 8	Q91048 gallus gall	rattus	P14781 gallus gall	rattus	_	Q06561 caenorhabdi
SUMMARIES	. OI	PTPF HUMAN	AXO1_RAT	AXO1_HUMAN	PGBM_MOUSE	PTPD_HUMAN	LAR DROME	NEOI RAT	NEO1 CHICK	NEO1 HUMAN	AXO1_CHICK	PTK7 HUMAN	DCC_MOUSE	NEO1 MOUSE	DCC_HUMAN	PGBM_HUMAN	NCM2 MOUSE	NRG_DROME	NCA1_CHICK	UN89_CAEEL	NRCA_CHICK	NCM2_HUMAN	KMLS_HUMAN	CAML_MOUSE	RAGE_BOVIN	NCA2_MOUSE	NCA1_MOUSE	CAML HUMAN	PTK7_CHICK	NCA1 RAT	CONT_CHICK	CAML_RAT	AMAL_DROME	UN52_CAEEL
	h DB	97 1	0	0	7 1	2	9	7	3	, ,	9	п 0	7	3	7	7	7	7	1	7	4	7	4		1	2	2	7	п П	1	0	9	3	2
	Length	18	1040	104	3707	191	2029	1377	1443	146	103	1070	1447	1493	144	4391	837	1302	1091	663	128	837	1914	126	41	72	111	125	1051	85	1010	1259	33	337
di	Query Match			•	•	•	15.1	•	14.6	•	4	4	4	4	•	•		•	•	•	•	٠		•	•			•	12.5	•	12.4		•	
	Score	23	230.5	228	225	222	222	221.5	215.5	214.5	213.5	212.5	209	209	206	203.5	202	199.5	195.5	195.5	194.5	-	191.5	191	186	185	185	185	184	m	182.5	m		181.5
	Result No.	-	N	e	4	5	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20		22		24			27	, 28	, 29	30	31	32	33

060469 homo sapien P31836 bos taurus O9bmus caenorhabdi Q03696 gallus gall P34082 drosophila P13592 homo sapien P13591 homo sapien Q15109 homo sapien Q12866 homo sapien Q28730 oryttolagus P12960 mus musculu
DSCA HUMAN NCAI_BOVIN NCAI_BOVIN NGCĀ CHICK FASZ_CROME NCAZ_HUMAN NCAI_HUMAN CONT_HUMAN CONT_RAT ICAS_RABIT CONT_MOUSE
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2012 853 2200 1266 873 761 848 404 1018 1021
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179 176 176 175 173.5 173.5 173.5 170.5 168 168 167.5

ALIGNMENTS

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DOMAIN
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                                                  57 PDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GAGSVLRIQP-----LRVQRDEAIYECTATNSLG-EINTSAKLSVL---EEEQLPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 RDMVAVVGEQF-----TLECGPPWGHPEPTVSWWKDGKPL--ALQPGR-HTVSGGS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GFPSIDMGPQLKVVEKARTATMLCA-AGGNPDPRISWFKDFLPVDPATSNGRIKQLRSGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 DŚKPVFIKVPEDÓTGLSGGVASFVCQATGEPKPRITWMKKGKKVŚSQRFEVIEFDD---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRWLLNGQPLS-----MVPPDPHHLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1538 BY SIMILARITY.
1829 BY SIMILARITY.
107 N-LINKED (GLCNAC. .) (POTENTIAL).
240 N-LINKED (GLCNAC. .) (POTENTIAL).
285 N-LINKED (GLCNAC. .) (POTENTIAL).
711 N-LINKED (GLCNAC. .) (POTENTIAL).
956 N-LINKED (GLCNAC. .) (POTENTIAL).
1538 C->S: LOSS OF ACTIVITY.
1, 211844 MW, 439850FID5C031FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%; Score 232.5; DB 1; Length 1897; 31.6%; Pred. No. 1.9e-10; trive 37; Mismatches 75; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
PIG-LIKE C2-TYPE 3.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                      PROSITE; PS503135; IG LIKE; 3.
PROSITE; PS503135; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_PRP; 2.
PROSITE; PS50050; Glycoprotein; 3ignal; Transmembrane; Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
LAR PROTEIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 LLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 199
          EMBL; Y00815; CAA68754.1;
PIR; S03841; TDHULK.
PDB; 1LAR; 25-APR-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                            Genew; HGNC:9670; PTPRF.
                                                                                                                                                                                                                                                       SMART; SM00060; FN3; 4.:
SMART; SM00408; IGC2; 3.
SMART; SM00194; PTPC; 2.
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nes 68; Conserv
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TRANSMEM
DOMAIN
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MUTAGEN
SEQUENCE
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RESULT 2

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                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: MAY PLAY A ROLE IN THE INITIAL GROWTH AND GUIDDANCE OF AXONS. MAY BE INVOLVED IN CELL ADHESION.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A GPI-ANCHOR AND IS ALSO RELEASED FROM NEURONS.
-i- TISSUE SPECIFICITY: IN NEURAL TISSUES IN EMBRYOS, AND IN ADULT BRAIN, SPINAL CORD AND CEREBELLUM.
-I DEVELOPMENTAL STRAES: TRANSIENTLY EXPRESSED ON A SUBSET OF AXONS IN THE DEVELOPING RAT NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTACTIN S.
CONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The axonal glycoprotein TAG-1 is an immunoglobulin superfamily member with neurite outgrowth-promoting activity."; Cell 61:157-170(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains. -!- SIMILARITY: Contains 4 fibronectin type III domains.
                       P22063;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)
(Transient axonal glycoprotein 1) (TAX-1)
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 31-41.
TISSUE-Spinal cord;
MEDLINE=90199890; PubMed=2317872;
Furley A.J., Morton S.B., Manalo D., Karagogeos D., Dodd J., Jessell T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0014; FNNYPEIII.
SMART; SM00060; FNN; 4.
SMART; SM00408; IGC2; 5.
PROSTIT; PSC8035; IG_LKE; 6.
Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
PRT; 1040 AA.
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PIR; A34695; A34695.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR003989; IG_C2.
InterPro; IPR003598; IG_C2.
InterPro; IPR003598; IG_C2.
STANDARD;
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SIGNAL
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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CARBOHYD
CARBOHYD
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13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 THEGWGVMLPCNPPAHYPGLSYRWLLNEPPNPIPTDGRHFVSGTTGNLYIARTNASDLGN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 YMCVATNSAGHRE-----SRAARVSI--QEPQDYT------EPVELLAVRIQLEN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 YSCLATS---HMDFSTKSVFSKFAQLNLAAEDPRLFAPSIKARFPPFTYALVGQQVTLEC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 V-VGEQFTLECGPPWGHPEPTVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEXT 177
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MEDLINE=91145965; PubMed=8425542;
MEDLINE=91145965; PubMed=8425542;
MEDLINE=91145965; PubMed=8425542;
"CDN Cloning, etructural features, and eucaryotic expression of human TAG-1/axonin-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=56163865; PubMed=8586412;
KOzlov S.V., Giger R.J., Hasler T., Korvatska E., Schorderet D.F.,
Sonderegger P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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     POTENTIAL)
                                                                                                                                                                                                                                                                                            DB 1; Length 1040;
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Q02246; P76432;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)
(Transient axonal glycoprotein 1) (TAX-1).
CONTAC OR TAXI OR TAG1.
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                        MW; 6E707EF6614CB4FB CRC64;
                                                                                                                                                                                                                                                                                                                 ; Pred. No. 1.3e-10; 41; Mismatches 98;
                                                                                                                                                           (GLCNAC.
                                                                                                          GLCNAC
                                                                               GLCNAC
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                                                                                                                                                                                                                                                                                            Score 230.5;
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                                                                                                                                                                                                                                                                                         15.6%;
28.8%;
                                                                                                                                                                                                                                        113042
                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 28.8
Matches 77; Conservative
  206
463
479
527
777
920
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942
1040 AA;
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SEQUENCE
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                                                                                                                               TISSUE-Placenta;
Taisoura C. P., Theodorakis C., Michaelidis M.T., Mamalaki C.,
Karagogeus D., Papamatheakis J.;
Submitted (NOV-1995) to the EMBJ/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN THE INITIAL GROWTH AND GUIDANCE OF
AXONS. MAY BE INVOLVED IN CELL ADHESION.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
GPI-ANCHOR AND IS ALES RELEASED FROM NEURONS.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 4 fibronectin type III domains.
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"The human TAX1 gene encoding the axon-associated cell adhesion molecule TAG-1/axonin-1: genomic structure and basic promoter."; Genomics 30:141-148(1995).
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Cell adhesion; Repeat.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C3-TYPE 6.
IG-LIKE C3-TYPE 6.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
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GO; GO:0005887; C:integral to plasma membrane; TAS.
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InterPro; IPR003962; FMIII subd.
InterPro; IPR007110; Ig-11Ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X68274; CAA48335.1; -.
EMBL; X67734; CAA47863.1; -.
EMBL; X95681; CAA63365.1; -.
EMBL; X84420; CAA59137.1; -.
EMBL; X85508; A49356.
HSSP; PQ10189; 1BQU.
Genew; HGNC:2172; CNTN2.
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SMART; SMO0060; FN3; 3.
SMART; SMO0408; IGC2; 5.
PROSITE; PS50835; IG LIKE; 6.
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Interpro; IPR003006; Ig_MHC.
Pfam; PF00041; fn3; 4.
Pfam; PF00047; ig; 6.
                                                                                                         SEQUENCE OF 1-136 FROM N.A.
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CARBOHYD
LIPID
SEQUENCE
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SIMILARITY:
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13;
                                                                                                                     LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                                                              95 LVIMNP-----TKAQDAGVYQCLASNPVGTVVSREAILRFGFLQE-FSKEERDPV 143
                                                                                                                                                                          -AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEX 176
                                                                                                                                                                                     144 KAHEGWGVMLPCNPPAHYPGLSYRWLLNBFPNFIPTDGRHFVSQTTGNLYIARINASDLG 203
                                                                                                                                                                                                                              TYMCVATNSAGHRE----SRAARVSIQ------EPQDYTEPVELLAVRIQLE 218
                                                                                                                                                                                                                                                      204 NYSCLATS---HMDFSTKSVFSKFAQLNLAAEDTRLFAPSIKARFPAETYALVGQQVTLE 260
                                                                 9
                                                                                         EDOPLSVI-PPEESTEE---QVILLACRARASPPATYRWKWNGTEMKLEPGSRHQLV-GGN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noonan D.W., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M., Yamada Y., Hassell J.R.;
Yamada Y., Hassell J.R.;
'Identification of CDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan.";
J. Biol. Chem. 263:16379-16387(1988).
-! FONCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.
-! SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type
                                                                 1 ODSPPOILVHPODOLFQGPGPARMSCRASGOPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M., Yamada Y., Hassell J.R.,
"The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion molecule."
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=89034110; PubMed=2972708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
protein precursor (HSPG) (Perlecan) (PLC).
             Length 1040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
PTW. CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: CONTAINS 4 LDL-receptor class A domains.
SIMILARITY: Contains 1 ll laminin EGF-like domains.
                                      99; Indels
            15.5%; Score 228; DB 1;
29.5%; Pred. No. 2.1e-10;
tive 38; Mismatches 99;
                                                                                                                                                                                                                                                                                                          261 CFAFGNPVPR-----IKWRKVDG 278
                                                                                                                                                                                                                                                                                219 NVTLLNPDPAEGPKPRPAVWLXW-KVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 266:22939-22947(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92078153; PubMed=1744087;
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
            Query Match
Best Local Similarity 29.54
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                           PGBM_MOUSE
005793;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE 1.
LAMININ EGF-LIKE 1 (N-TERMINAL).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal, Basement membrane, Proteoglycan, Repeat, Glycoprotein, Heparan sulfate, Laminin EGF-like domain, Immunoglobulin domain, Extracellular matrix, EGF-like domain, 3D-structure.
                    BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI: 66257; HSPG2.
GO; GO: 0005604; C: basement membrane; IDA.
GO; GO: 0008104; P: protein localization; IMP.
INCEPPO; IPR000742; EGF 2.
INCEPPO; IPR00110; IG-Tike.
INCEPPO; IPR003598; IG C2.
INCEPPO; IPR003598; IG C2.
INCEPPO; IPR003698; IG C3.
INCEPPO; IPR003698; IG MHC.
INCEPPO; IPR002049; Laminin EGF.
INCEPPO; IPR002049; Laminin EGF.
Contains 3 laminin IV domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LAM G DOMAIN; 3.
; LAMININ TYPE_EGF; 11.
; LDLRA_1; 4.
; LDLRA_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000082; SEA_domain.
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Pfam, PP00053; laminin EGF; 7.
Pfam, PP00054; laminin G; 3.
Pfam, PP00157; ldl recept a; 4.
Pfam, PP01390; SEA; 1.
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SMART; SM00180; EGF Lam; 7.
SMART; SM00408; IGCZ; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF 1; 8.
PROSITE; PS01186; EGF 2; 5.
PROSITE; PS50835; IG_LIKE; 15.
                                                                                                                                                                                                                                                                                                                                                  EMBL; M71174; AAA39911.1; -.
EMBL; J04054; AAA39899.1; -.
EMBL; J04055; AAA39912.1; -.
PIR; S18252; S18252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00281; LamB; 3.
SMART; SM00282; LamG; 3.
SMART; SM00192; LDLa; 4.
SMART; SM00200; SEA; 1.
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Pfam; PF00047; ig; 15..
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PROSITE, PS01248; L
PROSITE, PS01209; L
PROSITE, PSS0068; L
PROSITE, PSS0064; S
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PRIOR FILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-12
PRIOR PILING DATE: 1998-04-2
PRIOR PILING DATE: 1998-04-3
PRIOR PAPLICATION NUMBER: 60/08359
PRIOR PILING DATE: 1998-04-3
PRIOR PAPLICATION NUMBER: 60/08359
PRIOR PILING DATE: 1998-04-3
PRIOR PAPLICATION NUMBER: 60/08450
PRIOR PILING DATE: 1998-05-3
PRIOR PAPLICATION NUMBER: 60/08450
PRIOR PILING DATE: 1998-05-3
PRIOR PAPLICATION NUMBER: 60/08450
PRIOR PILING DATE: 1998-05-3
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                                                                                                                                                                                                                                                                       Length 985;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    88.9%; Score 1311; DB 11; 98.8%; Pred. No. 3.7e-100; ive 1; Mismatches 2;
          PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR APPLICATION NUMBER: 60/085689
PRIOR PLING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08550
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
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PRIOR PLING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085582
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Gurney, Austin L.
Hillan, Kenneth J
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Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                                         Conservative
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Eaton, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKVSGP 246
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Matches 243;
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R FILING DATE: 1998-05-05
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R FILING DATE: 1998-05-06
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R APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
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FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/083500
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APPLICATION NUMBER: 60/083742
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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APPLICATION UNDBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
                                                            PLICATION NUMBER: 60/081195
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FILING DATE: 1998-04-09
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PPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082804
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FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/084639
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FILING DATE: 1998-04-28
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TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TLE OF INVENTION: Acids Encoding the Same LE REFERENCE: P2630P1C17
                                                                     CURRENT APPLICATION NUMBER: 09/9184934
CURRENT APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 00/062250
PRIOR PILING DATE: 1090-10-10
PRIOR PILING DATE: 1090-10-10
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06249
PRIOR APPLICATION NUMBER: 60/06249
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-03-10
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-10
PRIOR PILING DATE: 1999-03-20
PRIOR PILING DATE: 1999-03-20
PRIOR PILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/07904
PRIOR PILING DATE: 1999-03-20
PRIOR PILING DATE: 1999-03-27
PRIOR PILING DATE: 1999-03-31
PRIOR PILING DATE: 199
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
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PRIOR FILING DATE: 2001-07-30
PRIOR PELICATION NUMBER: 60/06250
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-27
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R APPLICATION NUMBER: 60/079786

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079920

R FILING DATE: 1998-03-30

R APPLICATION NUMBER: 60/079920
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
FILING DATE: 1998-03-31
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-31
                                 Pan, Jámes
Paoni, Nicholas F.
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   Napier, Mary A.
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98.8%; Pred. No. 3.7e-100;
tive 1; Mismatches 2;
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                           DR APPLICATION NUMBER: 60/084643

DR FILING DATE: 1998-05-07

DR PILING DATE: 1998-05-07

DR PLING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/08523

DR FILING DATE: 1998-05-13

DR FILING DATE: 1998-05-13

DR FILING DATE: 1998-05-15

DR PLING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
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APPLICATION NUMBER: 60/085697
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Filvaroff, Ellen
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Gerber, Hanspeter
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Goddard, Audrey
FILING DATE: 1998-05-07
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Kuo, Sophia S.
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Best Local Similarity 98.8
Matches 243; Conservative
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APPLICATION NUMBER: 60/084639

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PRIOR FILING DATE: 1996-04-13
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR PLING DATE: 1996-04-12
PRIOR PLING
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121 AVVGEOPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
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Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2;
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PAPLICATION NUMBER: 60/084640
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084630
PRIOR APPLICATION NUMBER: 60/084627
PRIOR PILING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
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Desnoyers, Luc
Eaton, Dan
Perrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
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APPLICANT: Baker Kevin P.
APPLICANT: Boterein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napolec
APPLICANT: Ferrara, Napolec
APPLICANT: Filveroff, Eller
APPLICANT: Forg, Sherman
APPLICANT: Forg, Sherman
APPLICANT: Gao, Wei-Qiang
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US-09-999-833A-211
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-23
PRIOR PR
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/083500
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APPLICATION NUMBER: 60/083742
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                                                                                                                                                                                                                                                                                            PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                       Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
                                                                                                                                                                                                                            Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
                       rritsen, Mary E.
     Gerber, Hanspeter
                                                                                                                                                                                                              Paoni, Nicholas F
                                                            Sodowski, Paul J.
                                                                                                                                      Kljavin, Ivar J
                                                                                                                                                Kuo, Sophia S.
Napier, Mary A.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same
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CURRENT PRILICATION NUMBER: US/09/981,915A
CURRENT PILING DATE: 2001-10-16
PRIOR PAPLICATION NUMBER: US/09/9855
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065314
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PELING DATE: 1999-03-10
PRIOR PLING DATE: 1998-03-11
PRIOR PLING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-12
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Grimaldi, J. Christopher
Gurney, Austin L.
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/078936
FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR PLILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
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FILING DATE: 1998-03-13
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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                                                                                                                                        Ferrara, Napoleon
Filvaroff, Ellen
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Kuo, Sophia S.
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Gao, Wei-Qiang
                                        3otstein, Davi
                                                                                                      Eaton, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLINPDPAEGPKPRPAVWLX 240
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US-09-981-915A-211
Sequence 211, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
R APPLICATION NUMBER: 60/084366
RR FILING DATE: 1998-05-05
RR FILING DATE: 1998-05-06
RR FILING DATE: 1998-05-07
RR FILING DATE: 1998-05-07
RR APPLICATION NUMBER: 60/084637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R APPLICATION NUMBER: 6/085582
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 6/085700
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 6/085689
R FILING DATE: 1996-05-15
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/079728

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R APPLICATION NUMBER: 60/079923

R FILING DATE: 1998-03-30

R PILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080105

R APPLICATION NUMBER: 60/080107

R APPLICATION NUMBER: 60/080107

R APPLICATION NUMBER: 60/080165

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R APPLICATION NUMBER: 60/08037
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APPLICATION NUMBER: 60/082700
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082569
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FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/083322
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APPLICATION UNMBER: 60/083495
APPLICATION UNMBER: 60/083496
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APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/081071
           APPLICATION NUMBER: 60/
PILING DATE: 1998-03-27
                                                   FILING DATE: 1998-03-30
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LICATION NUMBER: 60/
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Pred. No. 3.7e-100;
1; Mismatches 2;
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R APPLICATION NUMBER: 60/084640
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084598
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084600
                                                                                                                                                                   FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
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FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/084637
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FILING DATE: 1998-05-07
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Search completed: January 30, 2004, 15:59:03 Job time : 29.1244 secs

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AK056544 Homo sapi
X17793 Mus musculu
BD085989 Method of
AF040990 Homo sapi
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AC16958 Mus muscu
AC138284 Mus muscu
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AC10983 Rattus no
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AF364048 Gallus ga
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AF337036 Danio rer
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AB046788 Homo sapi
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AF182037 Rattus no
BD085987 Method of
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AF040989 Drosophil
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1 QDSPPQILVHPQDQLFQGPG......SGPRLPREARELRGQRRNTG 276
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                                                                                          AlaValValGlyGluGlnPheThrLeuGluCysGlyProFroTrpGlyHisProGluPro 140
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PC AG1P29/00, AG1P31/04, AG1P31/12, AG1P35/00, C07K14/435, C07K16/18,
PC C12N1/15,
PC C12N1/15,
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PD 11-SEP-2001
PF 01-SEP-1994 JP 2000508394
PR 05-SEP-1997 US 60/057626,05-SEP-1997 US 60/057663 PR 05-SEP-1997 US 60/058667 PR 12-SEP-1997 US 60/058666
PL 12-SEP-1997 US 60/058666
PL PAUL A MOORE, SIEVEN M RUBEN, DAVID W LAFLEUR, YANGGU SHI, CRAIG
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Moore, P.A., Ruben, S.M., Lafleur, D.W., Shi, Y., Rosen, C.A., Olsen, H.S., Ebner, R. and Brewer, L.A.
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1. 1346

1. 1346

Location/Qualifiers

1. 1346

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/ a 379 c 376
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                   linear
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                  50 human secreted proteins
Patent: JP 2001514024-A 30 11-SEP-2001;
HUMAN GENOME SCIENCES INC
                   DNA
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                   1346 bp
                             50 human secreted proteins.
BD074325
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n equals a,t,g, or c
                                                             BD074325.1 GI:22619928
JP 2001514024-A/30.
Homo sapiens (human)
Homo sapiens
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JOURNAL
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/codom_start=1
/product="magic roundabout"
/product="magic roundabout"
/product="magic roundabout"
/product="magic roundabout"
/broduct="magic roundabout="magic roundabout"
/broduct="magic roundabou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huminiecki, L. and Bicknell, R.
Direct Submission
Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John Radcilife Hospital, Oxford OX3 9DS, UK
Location/Qualifiers
                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 3872)

Huminiecki,L. and Bicknell,R.

In sliico cloning of novel endothelial-specific genes

Genome Res. 10 (11), 1796-1806 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="endothelial-specific member of roundabout (ROBO)
        776 ACACTGCTGAACCCGGATCCTGCAGAGGCCCCCAAGCCTAGACCGGCGCGTGTGGCTCAGC
                                                                                                                                                                                                                                                                AF361473 3872 bp mRNA linear Homo sapiens magic roundabout mRNA, complete cds. AF361473
                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor family"
                                                                                                                                                                                                                                                                                                                                AF361473.1 GI:16930357
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Homo sapiens
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2 (bases 1 to 3872)
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RAARVSIQEPODYTEPVELLAVRIQLENVTLINPDPAEGPKPRPAVWISWKVSGPAAP
AOSYTALFRUGTAPGGGAPWABELLAGWGSAELGGHWGGDYFERKRRSESGRARGPD
SNVLLIRLPERKVPSAPPGGAPWABELLAGWGSAELGGHWGGDYFERKRRSESGRARGPD
SNVLLLALPERKVPSAPPGGATLKPFONTGAGAGABPRHNGIIRGYQWSLGNTSL
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PSEHGPWTLEQLRATLKRPEVIATGGTALMLLLGTAVCIHRRRARNHLGPGLYRYTS
EDAILKHRMDHSSOSQMLADTWRSTGSSRDLSSSSSLSSRGADARDPLOKTSLLSWD
SRSPGVPLLPDTSTFYGSLIALPESGTPARESPOVPAVRRLPPQLAGUSSPCSSSDSL
GSRGLSSPRLSLAPAEAWKAKKQELQHANSSPLLRGSHSLEIRACELGRRGSKNLS
QSPGAVYDALVARMALGPKLLSSSNELVFRHLPPAPLFPRHTPYGSQCTOPPVAPQA
PSSTILLPAAPIPILEPCSPSPPSPQASSLGSPSSRLSSSSSLSSLGBODSVLTPEEV
ALCLELSEGGETPRNSVSPMPRAPSPPTTYGYISVPTASEFTDMGRTGGGVGPKGGVL
LCPPRRECLTPPTSEGSLANGWGSASENDNAASARASIVSSSSGSFLADAHFARALAVAV
DSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLPIWEWRPDWLEDMEVSHTQRL
GRGMPPWPDGOISSQRGCHCRMPKAGASPVDYS"

1101 c 927 g 611 t
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                                                                                                                                                                                                                                                                                                                                                                                                                       JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, CHIAKI SENO,
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Funahashi,S., Seno,C. and Nezu,J.

Novel genes encoding protein kinase or protein phosphatase
Patent: WO 0109345-A 11 08-FEB-2001;
HELLX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
KOJI HAYASHI, KADAKU SALTO, JUNICHI YAWAWOTO, SHIZUKO ISHII, OMOYASU
SUGIYAWA, AI WAKAWATSU, KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI
FUNAHASHI, HIAKI SENO, JUNICHI NEZU
OS HOMO SAPIENS (human)

N WO 0109345-A/11
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                                                                                                                                                                                                                                                            PF 28-JUL-2000 WO 2000JP005060
PR 29-JUL-1999 JP 99P 248036,11-JAN-2000 JP 00P 118776
02-MAY-2000 JP 00P 183767,18-OCT-1999 US 60/159590 PR
17-FEB-2000 US, 78KAO ISOGAL, TETSUO NISHIKAWA, KOJI HAYASHI,
KAORU SAITO,
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/organism="Homo sapiens"
/mol type="genomic DNA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4263)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 4262)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 15015 09-JUL-2002;
                                                                                                                                                                                                                                                                                4262 bp DNA linear · PAT 17-JAN-2003 full-length cDNA and use thereof.
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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ACAGTCTCATGGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG
                 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys
                                                        ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
1333 c 1209 g 847
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BD160172.1 GI:27865930
JP 2002191363-A/15015.
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4262 bp mRNA linear PRI 01-AUG-2002
Homo sapiens cDNA FLJ14946 fis, clone PLACE2000034, weakly similar
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Rujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Rujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
M. Published Only in Database (2001)
2 (bases 1 to 186971)
25 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Rujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
M. Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Taurumi, Ku, Yokohama, Kanagawa 230-0045, Japan
TC-181-181-185503-9111, Fax:81-45-503-9170)
On Mar 7, 2002 this sequence version replaced gi:13603460.
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Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664121,
complete sequence.
          CTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAGGCCCAGTCCACA 360
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Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. NEDO human cDNA sequencing project

Lupublished

S (bases 1 to 4262)

S Isogai,T. and Otsuki,T.

Direct Submission

Ninetted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarau, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3955, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA library construction, S-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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                                                                                                                                ArgalaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHis 188
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1 (bases 1 to 3467)
Strausberg, R.

Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                31011 AGCCCTATCCTCCCCACAGAGCCCCAGGAGTACAGGGGGGCTGTGGAGCTTCTGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 ArgileGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro
                                            31491 TTTGAGGAGGGAGAGCAGGGGCCTCAAACTTCCCCCCAGCTCAGAGCCCCTCCCCACA
                                                                                                    31431 TAGGAGACTTCACAGTGAACCTGGCCCTGACAGGTCCGGGGGGTCCCTGCTGATGGCA
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Homo sapiens, clone IMAGE:4850025,
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                                                                                                                                                                                                                                                            GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly
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                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RR11-664121"
6 a 38908 c 40035 g 58382 t
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1232.50
48.46$
48.28$
83.56$
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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1 (bases 1 to 2886)
Roberts, K.G. and Stewart, L.M.
Direct Submission
Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England ECIA 7BE, United Kingdom
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trainiation="MGGEELRAAVDSGGMGLLGTKCPLPLLLLFIMGGKALDSPPQI
VPPPQPQLGGSGPARMSCRASGQPLPTIMILLACPLSMATPDLHYSOBGTLLLHR
PPHTARPQDDGDNILSALLGYVTERSNRLGTRAVSRARLSVATQEDFRIQPTVAV
VGESLVLECCPPWGYPKPSVSWWKDGKPLVLQPGKRTVSGDSLMVARAEKNDTGTYMC
WATNNAGQERSERAARVSIGESPBHKEHLLELLAVRIQENTLANPEPVKSPKCPRYNC
LSWKYSGPAAPAQSTALFRAQRDPRDQGSWTEVLLDGLLNAKLGGLRWGDNYEFV
RPSSGRARGPDSNVLLILRLPEQVPSAPPQGSTTRRPGNGSVFVSWAPPPABNHNGFIRG
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SQABGQSABDSAHSVBYTLEQIRATIKRPEVIASGAVILMILLILGIAVCIYRRRKAGV
HLGPGIXRYTSEDAILKHRWDHSDEPWILDYRRSTGGSRDISSSSSILSRIGYDPRD
LDGRRSIISWDPRSPGUPILLPDTSTFYGSLIAEQTSSPPVRPSPQTPAARRLPPKITG
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ELGSRASKNLSQSPGPNTCSPREAPGAVVAWRALGPQLHRNSSELAARPLPPTSLR
GAPSHDPQSQCVEKLQAPSSDPLPAAPLSVLNSSRPSSPQASFLSVPSPGSSSNLSSSS
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'gene="Robo4"
'note="ROBO4-1; similar to Homo sapiens and Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                       542 GTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCCCCAATCTTACACGGCCTTG
                                                422 TCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGGAGCTTCTGGCTGTGCGAATTCAG
                                                                                                            LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla
                                                                                                                                         237 ValTrpLeu***TrpLy8ValSerGlyPro***-ArgLeuProAsnleuThrArgProCy
                     SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln
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mRNA, complete cds.
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/gene="Robo4"
/note="Region: immunoglobulin domain"
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/db_xref="taxon:10116"
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/gene="Robo4"
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                                                         Contact: MCC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAL plate: 34 Rows a Column: 19.

Location/Qualifiers
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31 Center Drive, Room 11A03, Bethesda, MD 20892-2590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAC
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                                             URL: http://mgc.nci.nih.gov
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Conservative:
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clone lib="NIH MGC_113"
lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4850025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pOTB7"
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98.16%
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Best Local Similarity:
Query Match:
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756 bp DNA linear PAT 17-JAN-2003 full-length CDNA and use thereof.
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1 (bases 1 to 756)

2 (bases 1 to 756)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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      ATCCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTGGGCACAGCAGTGAGCCGGGGT 414
                                                160
                                                                                                                                                                                                                                                                            594
                                                                                                                                                                                                                                                                                                                      SerGlyGlySerLeuLeuMetAlaArgAlaGluLyBSerAspGlu***ThrTyrMetCyg 180
                                                                                                                                                                                                                                                                                                                                                                  654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  835 TGGAAGGTGAGCCCCTGCTGCACCTGCCCATACACACCCTGTTCAGGCGCAG 894
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TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                TCTGGGGATTCTCTGATGGTGGCAAGAGAAGAAGAAGAATGACGGGGACCTATATGTGT
                                                                                                                                       AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro
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Location/Qualifiers
1. .756
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JP 2002191363-A/5069
09-JUL-2002
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BD150226
BD150226.1 GI:27855984
JP 2002191363-A/5069.
Homo sapiens (human)
Homo sapiens
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Primer for synthesizing
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ACCESSION
VERSION
SEYMORDS
SOURCE
ORGANISM
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AUTHORS
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acid change"
'replace"c"
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072. .1329
gene="Robo4"
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                                                                                                                                                                                 note="Region: immunoglobulin-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin-like domain"
166. .384
/gene="Robo4"
/note="Region: immunoglobulin domain"
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Matches:
Conservative:
Mismatches:
Indels:
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/replace="a"
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                                                                                                           /note="Region: 169. 429
/gene="Robo4"
                                                                                                                                                                                                                                                                                                                                                                                                            472. .693
/gene="Robo4"
/note="Region: 3
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/gene="Robo4"
                                                                     169. .432
/gene="Robo4"
                                                                                                                                                                                                      .69. .396
gene="Robo4"
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gene="Robo4"
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gene="Robo4"
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'qene="Robo4"
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gene="Robo4"
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Lablabed Only in Database (2002)

12 (Dases 1 to 4694)

13 (Dases 1 to 4694)

14 (Daya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O. Direct Submission

15 Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research

16 Institute, Department of Human Gene Research; 1532-3, Yana,

17 Institute, Department of Human Gene Research; 1532-3, Yana,

18 Institute, Department of Human Gene Research; 1532-3, Yana,

18 Institute, Department of Human Gene Research

18 Institute.

18 Institute.

19 Institute.
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/product="FLJ00236 protein"
/protein id="BAB84989.1"
/db_xref="G1:18676674"
/translation="MSSGGDSLLGGRGSLPLLLLLIMVLREDPQIQPRDMVAVVGEQF
TLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCVAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLSWKV
SPAAROGSYTALFRYDARGGGGARMARELLAGWGSALGHWGQDYETKRRPSSG
RARGPDSNVLLLRLERVBARPQEVTLKPGRACYBVGARMYPPPARHNGIIRGYQWS
LGNTSLPPANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEGAME
RATQBSEBEHFWTLEQLRATLKRPBTATGCYALMLLLLGTAYGTHRRARRYHLGPG
LYRYTSEDAILKHRWHSDSQWLADTWRSTGGSRDLSSSSSSSSSSSSLSRLGADARDELDCRR
SLLSWDSRSPGVPLLPDTSTFYGSLIAELPSSTPARPSPQVPAVRRLPPQLAGLSSPC
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GSKNLSQSPGAVPQALVAWRALGPKLLSSSNELVTRHLPPAPLFPHETPPTQSQQTQP
PVAPQAPSSILLPAAPIPILSPCSPPSPQASSLSGPSPASSRLSSSSLSSLGEDQDSV
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 nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="FLJ00216"
/note="Start codon is not identified."
/codon_start=1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/note="vector:pBluescriptII
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                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FLJ00236"
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1446 c 1251 g 1
                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="spleen"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/gene="FLJ00236"
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869.00
96.49%
95.91%
58.92%
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DB:
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                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
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                                      JOURNAL
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 TITLE
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                                                                                                                                                                                                                                                                                                                   121 CAGGACTCCCCCCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGC 180
                                                                                                                                                                                                                                                                                                                                                                                          AspLeuGlyValTyrThrCysGluAlaSerAsnArgJeuGlyThrAlaValSerArgGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GCTCGGCTGTCTGTGGCTGTCCTCCGGGAGATTTCCAGATCCAGCCTCGAGACATGGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                     ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 TCCGGGGGGCTCCCTGCTGATGGCAAGAGCAGAAGAAGAGTGACGAAGAGGGACCTACATGTGT
                                                                                                                                                                                                                                                                                              GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly
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                                                       3 others
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205
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens mRNA for FLJ00236 protein.
                                                       u
                                                       128
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
. 242 c 236 g 12
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fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                                                                                                            2.82e-54
1057.00
97.17%
96.70%
71.66%
                                                                                                                                                                                 Best Local Similarity:
Query Match:
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                                                                                                            Alignment Scores:
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ACCESSION
VERSION
KEYWORDS
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                                                     BASE COUNT
ORIGIN
                                                                                                                                 No.
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AUTHORS
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Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melorim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., O'Connor, T., O'Donnell, P., O'Meil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbe, K., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbe, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasailiev, H., Venkataraman, V.S., Vael, R., Vo, A., Wilson, B., Wu, X., Wman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Max 4, 2003 this sequence version replaced gi:28201704. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 207512 bases at least Q40 Consensus quality: 207512 bases at least Q30 Consensus quality: 207947 bases at least Q30 Insert size: 182000; agarose-fp Insert size: 208212; aum-of-contigs Quality coverage: 11.1 in Q20 bases; sum-of-contigs Quality coverage: 9.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 38270 bp in length
contig of 1220 bp in length
gap of 1220 bp in length
gap of 100 bp
contig of 7484 bp in length
gap of 100 bp
contig of 14344 bp in length
gap of 100 bp
contig of 24381 bp in length
gap of 100 bp
contig of 26307 bp in length
gap of 100 bp
contig of 26307 bp in length
gap of 100 bp
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
of 29749 bp in length
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of 35882 bp in length
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/clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .209012
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L19390
Center clone name: 325_P_4
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38370:
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86099:
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                                        183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202
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JOURNAL Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 23, 2003 this sequence version replaced gi:28460994. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html	**NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as true of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. ** This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. ** This secret is available and the accession number will stand to the preserved. ** This secret is available and the accession number will stand in 134271 is available and the accession number will stand in 134271 is available and the accession number will stand in 134271 is available and the accession number will stand in 134271 is available of 100 bp ** 134171 is available of 100 bp ** 159138 129137; gap of 100 bp ** 159138 129137; gap of 100 bp ** 159138 129137; gap of 100 bp ** 121280 121279; contig of 2180 bp in length ** 121280 121279; contig of 2180 bp in length ** 1214559; contig of 2180 bp in length ** 1214559; contig of 2180 bp in length ** 1214559; contig of 2180 bp in length ** Accation/Qualifiers // Ab_xref="taxon:10090"	// map=19" // map=19" // map=19" // map=19" // map=19" // clone="RP3-35cD13" // clone="RP3-35cD13" // clone="Ib="RPCI-23 Female Mouse BAC" // clone=massembly_fragment // clone=massembly_fragment // misc_feature // clone=massembly_fragment // misc_feature // clone=massembly_fragment // // // clone=massembly_fragment // // // // // // // // // // // // //
Oy 243	REFERENCE 1 (bases 1 to 214559) AUTHORS Birren, B., Nusbaum, C. and Lander, E. AUTHORS Birren, B., Nusbaum, C. and Lander, E. JOURNAL Dipublished 2 (bases 1 to 214559) Birren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, B., Choepel, Y., Collymore, A., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Ferrer, N., Hafez, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., MacDean, C., MacDean, C., Machand, P., Mathews, C., McCarthy, M., Meditim, J., Maneus, L., Mihova, T., Mathews, C., McCarthy, M., Meditim, J., Meneus, L., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Lonnell, P., O'Lonner, T., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Steper, F., Saman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Taefaye, S., Theodore, J., Topham, K., Travers, M., Wagan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	RS

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ογ 199 199	Db 187564 TAATAAGGGCTCAGAAGAACTCTGTGGGGTAAGGTGCTGCCTTCACATACGTGAAGAGT 187505	187504 CAAGTTCTCCAGCACTCATATAAAAGCAGAGTGTGACAGTGAATGTCGATCATCCCAGTG 18	CCGATGTGGAGAACAGACAGGTGAATCCCAGAAGCTAACCAGACAGA	199	199	187264 CACTCAAAGTTCAAGGTAAGGTAGGAGACTCCAGTTAGTGTGCTCACCAGGTATGGAGTT	Db 187204 TGGGGTCCAAGTGATGAGGCCAAATGGGATACTCCAGAGCTGAAAACTCTGGG 187145	187144 AGCCAAGTTTGTCCACGATGAAGGTATGTTCCACTACTCCATCCCAGTCCTGTGTTCCTC	Oy 200GluProGlnAspTyrThrGluProValGluLeuEavalArg1leGlnLeuGl 218	Oy 218 uAsnValThrLeuLeuAsnProAlagProAlaGluGlyProLysProArgProAlaValTr 238	238 pleu***TrpLys	Db 186964 GCTCAGCTGGAAGGTGAGACAGAGGTCCCAGAAACACCCCAGAGCTCAGATTAGGGCTGC 186905	186904 CATGAGCTCCCTAGTCCATTATCGTTGCTCTGACTTCTTCCCAGGTGAGCGGCCCTGCTG	Oy 248 ArgleuProAsnLeuThrArgProCysSerGlyProArgLeuProArgGluAlaArgGlu 267	Oy 268 LeuargGlyGlnarg 272 	RESULT 14 ACT20636/C 223269 bp DNA linear HTG 20-NOV-2002 LOCUS DEFINITION Rattus norvegicus clone CH230-136D4, *** SEQUENCING IN PROGRESS	ACCESSION AC120636 VERSION AC120636.4 GI:25138029 KEYWORDS HTG; HTGS PHASE2; HTGS ENRICHED.	NISM Rattus norvegicus Eukaryota; Metazoa Mammalia; Butheria	REFERENCE I (bases 1 to 223269) AUTHORS Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., AUTHORS Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Best Local Similarity: 33.61% Mismatches: 43 Query Match: 56.10% Indels: 336 DB: 5	US-10-047-021-86_COPY_28_303 (1-276) x AC138284 (1-214559)	Qy 2 AspSerProBroGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21	Oy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeuAsn 41	Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61	Qy 62 LeuLeuGLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80	Qy 81 AspleuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100 	Oy 101 AlaargLeuSerValAla	Qy 106 106 Dh 188224 GCTGAGATGTTTGTTCGAGGAATACGAGAGTTTGTGAAGGGAAGGAA	106	DD 188164 AGGGTCTTGGGATGGAGAACTAGGTTAAACTAGAGAGGGCAAGGAAGTGGTAGAG 188105 Qy 106 106	Db 188104 CAGAATTGGGTAAGCATGTTCGGATAAGCCATCCATGTTAGGATTTAGAAGGACTCAGG 188045 Qy 107	Db · 188044 GTGGGTAGACGTGCTTCCTGCTGATTTGCTGACTTCCCAATAGTCCTCCAGAGGACTTC 187985	Qy 113 GInīleGinProArgAspMetValAlaValValGiyGluGinPheThrLeuGluCysGly 132 	Qy 133 ProProTrpGlyHisProGluProThrValSerTrpTrpLysAspClyLysProLeuAla 152	Qy 153 LeuGlnProGlyArgHis	Qy 158 158 Db 187804 ATCATCCTGTGCACATTGAGCAACTGACCCACCTCCAACCTCTAAGCTTCTCAA 187745	Oy 159	Oy 168 aArgalaGluLysSerAspGlu***ThrTyrMetCysValalaThrAsnSerAlaGlyHi 188 ::	Oy 188 sArgGluSerArgAlaAlaArgValSerIleGln

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Raddiche, W. 1814: A. Blankenberg, K. 1814. Bennicad, M. Banden, H., Balddich, D., Watter, B. Mayolebesh, V., Darcer, J. Blankenberg, K. 1814. M. Bandersad, M. 1814. Blanken, M. 1814. Blanken,
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TITLE JOURNAL REFERENCE TITLE JOURNAL

AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 22269: contig of 223269 by in length.
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                                                                                                                        Center project Information
Center project name: GXDD
Center clone name: GXDD
Center clone name: GXDD
Assembly program: Phrap; version 0.990329
Consensus quality: 201827 bases at least Q40
Consensus quality: 2047782 bases at least Q30
Consensus quality: 206701 bases at least Q30
Eximated insert size: 209571; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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a 47952 c 46732 g 54018 t 15157 others
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                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
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Matches:
Conservative:
Center: Baylor College of Medicine
Center code: BCM
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    .223269
    /organism="Rattus norvegicus"

                                                                                                  Contact: hgsc-help@bcm.tmc.edu
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/db_xref="taxon:10116"
/clone="CH230-136D4"
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104879, .106665
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164341. .165851
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Db 201412 TGTCTCACABABACAGGAGGAACAGGAGGAGCTTTTGGCTTCCATAGCCAC 201553 0y 199	Anyalebechi, V., Aoyagi, A., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Banahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dapan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Garcia, A., Garre, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harnandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulw, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R., Jolivet, A.,
	Db 201712 GGGALCTATTGTGTATGGCCAACAATGCCGGACAACAGGGAGAGTCGGGAGACCCAGG 201653 Oy 196 ValSerIleGln

NOTE: This is a 'working draft,' sequence. It currently

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On Nov 15, 2002 this sequence version replaced gi:23366067.
The sequence in this sequencing reads assembled using Atlas and whols genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold; individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Karpathy, S., Kelly, S., Khly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulesged, H., Lozado, R.J., Lu, X., Ma, J., Mannadarto, M., Mahmoud, M., Martinez, E., Mapca, J., Mapta, P., Martin, R., Martinez, E., Mapca, P., Martin, R., Martinez, E., Mapca, P., McLeod, M. P., McNeill, T.Z., Meenen, E., Mores, S., Moredam, M., Morris, S., Morris, S., Munidasa, M., Murphy, M., Nair, L., Markervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasterrak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Parks, K., Pasterrak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reeves, K., Regier, M.A., Reigh, R., Reilly, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneeth, N., Strong, R., Walzer, P., Wallsen, R., Warren, Z., Wooden, H., Worley, K., Wright, D., Wright, R., Weise, R., Strong, R., Stro
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Rat Genome Sequencing Consortium.
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Center: Baylor College of Medicine
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129886 GATTCTCCCCCCCAGATCCTAGTTCATCCCCAGGACCAGGTACTTCAGGGCTCCGGGCCG 129945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129946 GCCAAGATGAGTTGCAGAGCATCGGGCCAACCACTTCCCACTATCCGTGGCTGCTGCTGAAT 130005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AppLeuGlyValTyrThrCygGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly
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consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 250318: contig of 250318 bp in length.
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249161. .250318
hote="wage and_extension
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51524 c 51351 g 66227 t 14275 others
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Conservative:
Mismatches:
Indels:
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ą	130245	GGCTGCGATGTTTGTGTCCAAGGAAATACGAGGGTCTATCTA	130304
≿	106		106
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ą	130365	TGGGTAAGCGCGTTAGGATAAGCAAAGGACTCGGGGTGGGT	130424
ð	130425		
≿		AlavalValGluGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro	
ð	130485		130544
≿	141	ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThr	159
g	130545		130604
≿:	159		159
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ą	130725	GAGACCTCAAATTGCCCTCCGCCCTCTAAGTTTCTCACACTGAAGATTTCATGGAGTATT	130784
≿	160		
q	130785		130844
≿		***ThrTyzMetCysValalaThrAsnSerAlaGlyHisAzgGluSerAzgAlaAzg	
ဂ္ဂ	130845		130904
≿	196		199
ď	130905	GTGTCTATCCAGGGTAAGGACAGGAGTCATCTAAAATCCAATAAGGGCTCAGGAGATAAC	130964
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ą	130965	TCTGTGTGTAACATGCTTGCTTCATATATGTGAAGACTCAAGCAGCCCAGGACCCATATA	131024
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ą	131145	TGTCTCACAAAAAACAAGATGGAGAACAGCAGTAAGGGAGCTTTTGGCTTCCATAGCCAC	131204
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ą	131205	GCTCACTCACATACACACGTGTGAACCCACACTCAAAGTGCAAGGCAAAGTAGGAGACTC	131264
≿;	199		199
ą	131265	CAGITAGTGTGGTGGCCAGGTATGGGGTTCAGGGTCCTCCCTATGTGAGGCTAGAACGCA	131324
≿:	199		199

qq	131325	131325 CATAGGAATACTCTAGACCTGGAAACTCTGGGAGCCAAGTTTATCCAAGATGAAGATAGG 131384	131384
ò	200	GluProGlnAspTyrThrGluPr 	207
qa	131385	131385 ITCCACTCCTCCATCCCATCCCTGTGATCTCCCCACAGAGTCACCGGACCAAGGAGCA 131444	131444
ò	207	207 oValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspPr	227
요	131445	131445 TCTAGAGCTTCTGGCTGTTCGAATTCAGCTGAAATGTGACCCTGCTGAACCCAGAACC 131504	131504
ò	227	227 oAlaGluGlyProLysProArgProAlaValTrpLeu***TrpLys	242
අු	131505	131505 TGTAAAAGGCCCCAAGCCTGGGCCAGCTGTGTGTGGAAGGTGAGGCAGAGGAC 131564	131564
ò	242		242
ą	131565	131565 CCTGAAGACACGGAGGCTCCCATGGACTCCCTAGTTCCCTGTCCTTACTCTGACCTCTC 131624	131624
ò	243	ValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProArg	260
q	131625	131625 CCCAGGTGAGCGGCCCTGCTGCACCTCCAGTCATACACAGCCCTGTTCAGGCGGCAGA 131684	131684
ò	261	261 LeuProArgGluAlaArgGluLeuArgGlyGlnArg 272	
q	131685	131685 GGGACCCCAGGGACCAGGGATCTCCATGGACAGAGG 131720	
Sear	ch complet time : 315	Search completed: January 31, 2004, 14:37:34 Job time : 3137.42 secs	

Run on:

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Human secreted protein; cancer; immune disorder; infection; inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disorder; arthritic disorder; asthma; immunodeficiency disease; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                SUMMARIES
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AAX57252
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                                                                                                                                                                           January 31, 2004, 11:37:09 ; Search time 220.228 Seconds (without alignments) 3383.062 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                       - nucleic search, using frame plus p2n model
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1 QDSPPQILVHPQDQLFQGPG.....
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Listing first 45 summaries
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Drosophila Robo I Drosophila sp. ROB Drosophila melanog C. elegans ROBO po C. elegans ROBO co Drosophila melanog Drosophila sp. ROB Drosophila sp. ROB Drosophila melanog

Human p53 target m Human cDNA differe Gene #1758 used to

Angiogenesis-assoc Human peroxidasin Human bone remodel Melanoma associate Human osteoblast d Human cytoskeleton Human secreted pro Drosophila melanog Human transient ax Human cDNA encodin

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Human T85 cDNA.

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Description

and is derived by analysis of the total score distribution

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100 411 120 200

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831

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ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
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CITCIGCTACAGCCCCTGCCCGGGGACATGCCCACGATGGCCAGGCCCTGTCCACA 351
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                                                                                                                                                                   AlavalvalGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro
                                                                                                                                                                                                                                            ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX51701-55 encode human secreted proteins. The polymucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are presence of mutations in the new polymucleotides by determining the presence of mutations in the new polymucleotides. Specific uses are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, number disorders, atherosclerosis, restenosis, skeletal disorders, neurological disorders, arthritic disorders, selection, the polypeptides are also useful for identifying their rejection.
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                                                                                                                                                                                                                                                                                       Olsen HS;
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Shi Y;
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970S-0058666.
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P-PSDB; AAY12934.
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                                                                                           New polynucleotides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or
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             Rosen CA,
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Matches:
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             Shi Y,
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             LaFleur DW,
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           Ruben SM,
Brewer LA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys
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                                       ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
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Yang Y, Wehrman T, Drmanac
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P-PSDB; ABB97310.
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ABNS 1110

ABNS 1
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(first entry)

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Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 other;
                                                                                                  cDNA human ECSM4 protein.
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268
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The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, the manufacture of diagnositic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac disease, or endometricals by detecting the amount of ECSM4 proteins are useful in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atheroselerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
Human; endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
70..3384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 12; 248pp; English.
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/product= "ECSM4"
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P-PSDB; AAU99419.
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US-10-047-021-86_COPY_28_303 (1-276) x ABK87137 (1-3715)

ABK87137 standard; cDNA; 3715 BP.

Length: Matches: Conservative: Mismatches: Indels: Gaps:

8.42e-88 1432.00 98.53% 98.17%

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to tract a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA23891 to AA234338, and AAY41685 to AAY41774 represent polynucleotide and invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
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98US-0085338.
98US-0085539.
98US-0085573.
98US-0085580.
98US-0085682.
98US-0085682.
98US-0085700.
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P-PSDB; AAY41716.
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Best Local Similarity:
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18-MAY-1998;
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    AlavalvalGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro
                      GCTGTGGGGGGGGGGGGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC
                                                                                   ACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACTG
                                                                                                                                                                                                                        Gregocaccaacaeceaegacaraegaagaegecececeaecceeegrrrccarccaegae
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                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAAGGTCAGTGGCCCTGCCCTGCCCCAATCTTACACGCCCTTGTTCAGGACCCAG
                                                               Thr ValSer Trp Trp Lys AspGly Lys ProLeu Ala Leu Gln ProGly ArgHis Thr Val
                                                                                                                                                           ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia; cardiac insufficiency; nervous system disorder; kidney disorder; bone disorder; cartilage disorder; arthritis; tumour; wound healing; genetic disorder; cytostatic; antidiabetic; antiinflammatory; antiathritic; anti-tumour; vulnerary; antianaemic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO polypeptide; secreted and transmembrane protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human PRO860 polypeptide.
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30-NOV-1999; 99W0-US28313.
02-DEC-1999; 99W0-US28551.
02-DEC-1999; 99W0-US30095.
16-DEC-1999; 99W0-US30095.
30-DEC-1999; 99W0-US31243.
30-DEC-1999; 99W0-US31274.
05-JAN-2000; 2000W0-US01277.
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99WO-US00106.
99WO-US05028.
99WO-US05190.
99WO-US10733.
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                                                                                                                                                                                                                                                                                                                                                                                                              Bequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polyucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting and be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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                                                                                                                                                                                                                                                                                                   Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                                                        Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
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Indels:
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02-DEC-1999; 99WO-US28565.
16-DEC-1999; 99WO-US31095.
30-DEC-1999; 99WO-US31243.
30-DEC-1999; 99WO-US31274.
05-JAN-2000; 2000WO-US02279.
06-JAN-2000; 2000WO-US0277.
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P-PSDB; AAB44272.
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25-AUG-1999;
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The present invention relates to the isolation of novel human PRO polypoptides, and the polymucleocide sequences encoding them. The PRO polypoptides are secreted and transmembrane proteins. The PRO polypoptides are useful for detecting other PRO polypoptides, for linking bioactive molecules to cells expressing PRO polypoptides, and for for identifying agonists or antagonists. The polypoptides, and for for identifying agonists or antagonists. The polypoptides, and for for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and causes bioactive molecule maybe a toxin, radiolabel or antibody, and causes cardiac immune disorders, diabetes or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system disorders, kidney disorders, cone and cartilage disorders or arthritis, tumours, and wound healing. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation. The sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic contact directly from the USPTO web site at
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                                                      Haker KP, Botstein D, Desnoyers L, Eaton D; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kuo SS, Napler MA, Pan J, Paoni NF, Roy MA; Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                         Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
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                                                                             Ferrara N, F
Goddard A, G
Kljavin IJ,
Shelton DL,
                                                        Ashkenazi A,
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ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
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P-PSDB; AAU00501.
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                                                                                                                                                                                                                         ACACTGCTGAACCCGGATCCTGCAGAGGCCCCAAGCCTAGACCGGCGCTGTGGCTCAGC 792
                                                                                                                                                                                                                                                   Human; TANGO 315; clone Jthxel81e12; TANGO 330; TANGO 437; TANGO 480; cellular process regulator; gene therapy; astrocyte; cancer; s8; Roundabout; adrenal cortex; Hypodrenalism; hyperadrenalism; neoplasia; cell proliferative disorder; neurological disorder; Alzheimer's disease.
                                                                                                                                                 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro
                                    GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC
                                                            Thr Val Ser Trp Trp Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val
                                                                       ACAGICTCATGGGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACGCA
                                                                                                           TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGGACCTACATGTGT
                                                                                                                                   ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu
                                                                                                                                                                                                                                          TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr
                                                                                                                                                                    ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
                                                                                                                                                                                                       ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "TANGO 330 form 2 protein"
/note= "The ORF is specifically claimed"
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                                                                                                                                                                                                                                                                                              Human TANGO 330 form 2 cDNA sequence.
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The present sequence encoding for human TANGO 330 form 2 is isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA isolated from cDNA clone Jthxe181e12 from a human transmembrane proteins which also includes TANGO 310 is 1 of a novel human transmembrane proteins and TANGO 480 (AAU00503). The nucleic acids encoding these proteins care useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acid molecules and containing the TANGO nucleic acids are also described. Diagnostic assays can be used to detect genetic alterations in the TANGO Diagnostic acids and to identify compounds that bind to or modulate activity concleic acids and proteins Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 310 shows homology to human Roundabout. TANGO 310 nucleic acids and proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat cell proliferative disorders (e.g. cancer), and neurological disorders e.g. Alzheimer's disease.
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Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
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oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are present allow obtaining of the full-length AH1363s and AH1363s to AAH1363s to AAH1363s and AAH364s represent human amino acid sequences; AAB92465 to AAH1363s represent unian amino acid sequences; and AAH1363s to AAH1363s represent oligonucleotides, all of which are used in the exemplification
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SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys
                                    ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu
                                                                                                                                                        ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
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Otsuki
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A, Nagai K,
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
Senoo C, Nezu J;
                                          841 TGGAAGGTCAGTGGCCCTGCTGCCCCAATCTTACACGCCCTTGTTCAGACCCAG
                   TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes encoding protein kinase and protein phosphatase, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes
                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a human protein kinase/protein phosphatase
                                                                                                                                                                                                                                                                                                                                                    Human; protein kinase; protein phosphatase; signal transduction;
intracellular signalling pathway; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "protein kinase/protein phosphatase"
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Matches:
Conservative:
Mismatches:
Indels:
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11-JAN-22000; 20000JP-0118776.
17-FEB-2000; 2000US-0183322.
02-MAY-2000; 2000UP-01833757.
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Best Local Similarity:
Query Match:
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Pred. No.:
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The present sequence encoding for human TANGO 330 form 1 is isolated from cDNA clone jthAa060g22 from a human adrenal gland contained from cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins are useful, as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acids are also described. CC Diagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids are used diagnostically to fethe TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 310 shows homology to human Roundabout. TANGO 310 nucleic acids of monitor proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat call proliferative disorders (e.g. cancer),
proliferative disorder; neurological disorder; Alzheimer's disease
                                                                                                                         'product= "TANGO 330 form 1 protein"
'note= "The ORF is specifically claimed. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     607 A; 1008 C; 859 G; 568 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders e.g. Alzheimer's disease.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                          note= "The ORF is
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P-PSDB; AAU00500.
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uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa

gececaggaerracaegageerrergagerrergeergreegaarreagerggaaaargr 220 lThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu**

342 180

CACAGTCTCATGGTGGAAAGATGGGAAACCCTTGGGCCCTCCAGCCCGGAAGGCACACAGT

oThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVa

egereregegreageaerrracreregaargregecegeceregegecaeecaagagee

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282 160

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162

AGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGG

CGCTCGGCTGTCTGTGGCTGTCCTCCGGAGGATTTCCAGATCCAGCCTCGGGACATGGT lalavalvalGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPr

yAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVa

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583 crista Adelica de recentra de contra contra de contr

*TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProA

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523 GACACTGCTGAACCCGGATCCTGCAGAGGCCCCCAAGCCTAGACCGGCGGTGTGGCTCAG

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Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; dlabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic;
GACTGCCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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note='"ECSM4 #2"
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/note= "ECSM4 #3"
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61 LeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerTh 80

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US-10-047-021-86_COPY_28_303 (1-276) x AAS01694 (1-3042)

Best Local Similarity:

Query Match:

Percent Similarity:

240 839

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ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
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                                                                                                                                          <u>eccercerceacada a contrativa a refredence recerce a contrativa a secencia a </u>
                                                                                                                                                                                             ThrValSerTrpTrpLy8A8pGlyLy8ProLeuAlaLeuGlnProGlyArgHisThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
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Otsuki
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A, Nagai K,
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T, Wakamatsu
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to endothelial cell-specific molecule 4 (BCSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, necvasculature) such as cancer, psoriasis, diabetic retinopathy, the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour necvasculature, cardiac citation, detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for medulating angigenesis in an individual. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro
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Conservative:
Mismatches:
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P-PSDB; AAU99420, AAU99421, AAU99422.
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74.73%
72.03%
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                                                                                                                                                                       2000US-245566P
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        WO200236771-A2
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181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
                                    661 GTGGC-ACCAACAGGGACACAGGGAGAGCCGNGCACC-CGGGTTTNCATTCAGGAG 718
                                                                                                                                                                                                                                                                                                                                                   T85; FHMB-6D4; FMHV-SD4; human; neurological disorder; therapy;
                                                                                                 ProGlnAspTyrThrGluProValGluLeuLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                              AAV69278 standard; cDNA; 4291 BP
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1018..3216
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958..1017
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P-PSDB; AAW83927.
                                                                                                                                                                                                                                                                                                                Human T85 cDNA.
                                                                                                                                                                                                                                                                                                                                                                       diagnosis; ss.
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Pred. No.:
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                                            Lull-length cDNAs defined in the specification. Where a primer sets comprises: (a) an oligo-dr primer and an oligonucleotide complementary comprises: (a) an oligo-dr primer and an oligonucleotide complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polymucleotide which comprises a 3'-end sequence complementary to a polymucleotide which comprises a 3'-end sequence complementary to a polymucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification. The primers are useful for synthesialng polymucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also wseful for AHH1363 and AHH13631 to AAH13641 to AAH13632 to AAH13631 represent human amino acid sequences; and AAH13629 to AAH13631 represent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
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                                        present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 756 BP; 147 A; 242 C; 236 G; 128 T; 3 other;
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205
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Matches:
Conservative:
Mismatches:
Indels:
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Claim 1; SEQ ID 5069; 2537pp + CD ROM; English.
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This claimed cDNA sequence, the coding region of which is also claimed, codes for novel human T85 (see AAM83927), also referred to claimed, codes for novel human T85 (see AAM83927), also referred to EMHB-6D4 and FWHB-SD4. The CDNA was identified in a human foetal brain cDNA library using a screen designed to identify genes caids and polypeptides of the invention are useful as modulating agents in regulating a variety of callular processes. They can be activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, foremsic biology), predictive medicine (e.g. tissue typing, foremsic biology), predictive medicine (e.g. diagnostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders.
New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
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                                                         US-10-047-021-86_COPY_28_303 (1-276) x AAV69278 (1-4291)
  Conservative:
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Percent Similarity:
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The invention relates to a method for modulating the amount of Comm (Commissureless) polypeptide in contact with a cell expressing active Robo (roundabout) on its surface. The method comprises modulating the effective amount of comm polypeptide in contact with the cell, where the amount of expressed active Robo is specifically modulated inversely with the medulation of the effective amount of Comm in contact with the cell. The method is used to modulate the amount of active Robo expressed on a cell. The method can be used to screen for agents that modulate Robo:Comm interactions. This is particularly useful for modulating nerve cell
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370 AGTGGATCTTTATTTTTTTACGT------ATAGTACATGGACGAAA 411
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                                         Russell
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                                                                                                                                             Disclosure; Page 42-44; 56pp; English.
                                         Mitchell KJ,
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                                          Kid T,
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- 712 TATGITITGIGITGGTACCAATATGGTTGGGGAACGIGAGGGGAAGTAGCCGAGCTGACT 771 Š 원

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Search completed: January 31, 2004, 12:48:19 Job time: 231.228 secs

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 2, Appli
Sequence 27, Appli
Sequence 1120, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 760, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 5, Appli
Sequence 28, Appli
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Sequence 22, Appli
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OTHER INFORMATION: Incyte ID No. 6426186 199882.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
US-08-427-497E-6
US-08-371-843B-1
US-08-427-497E-2
US-08-427-497E-2
US-08-505-296B-27
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US-09-506-485-1
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US-09-528-312
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US-09-620-312D-76
US-09-620-312B-6
US-08-633-148-3
US-08-633-148-3
US-08-633-148-3
US-08-648-420A-5
US-08-648-420A-5
US-08-644-271-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/09484970B
Fatent No. 6426186
GENERAL INFORMATION:
APPLICANT: JONES Karen A.
APPLICANT: Walker, Michael G.
TITLE REPERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT APPLICATION NUMBER: US/09/484,970B
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or other
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18.75%
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OTHER INFORMATION: a, t, c,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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     Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-MODEL=frame+p2n.model -DEV=xlp
-MODEL=frame+p2n.model -DEV=xlp
-DEFGDM2_I/USFTO spool p/US10047021/runat_30012004_145453_24595/app_query.fasta_1.910
-DE=ISBUEd_Patente NA -OFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINEN=0 -ALGN=200000000
-USER=LOCAL -OUTFNT=pco -NOSM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=USIO047021_0CGN 1 1 133 @runat_3 30012004_145453_24595 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2, Appli
Sequence 132, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                         January 31, 2004, 12:35:25 ; Search time 60.5389 Seconds (without alignments) 2012.290 Willion cell updates/sec
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                                                                                                                                                                                                                                     1 QDSPPQILVHPQDQLFQGPG.....SGPRLPREARELRGQRRNTG 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2 6/ptodata/2/ina/5A COMB.seq:*
/cgn2 6/ptodata/2/ina/5B_COMB.seq:*
/cgn2 6/ptodata/2/ina/6A COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                         nucleic search, using frame_plus_p2n model
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US-08-447-464-2
US-08-716-679-2
US-09-016-434-1132
US-08-348-006B-6
US-08-800-825A-6
US-09-125A-6
PCT-US94-1016-6
US-09-538-6513
US-09-041-886-24
PCT-US94-0527-1
US-09-638-649-2
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                                                                                                                                                                                                                                                                                                                                                                                569978 seqs, 220691566 residues
                                                                                                                                                                                                US-10-047-021-86_COPY_28_303
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                        Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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2218.5 2118.5 2218.5 2206.5 206.5 206.5 206.5 206.5 206.5 206.5 206.5 206.5 206.5 206.5 206.5

Result No.

1155 Avenue of the Americas

New York U.S.A.

New York

10036-2711

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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570.
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 761
TELECOMMUNICATION:
TELEPHONE: 212-790-9090
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 5690 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                               CITY: Nev
STATE: Ne
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1174 TCCTGGACGAGGAGGAGGACGCACCTTGCCAGTTGACCGGGGGGGACATCACGCCT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1294 GCGACCAACAATTGACAGCGTCCATGCCACGCTTTCATCATCGTCCAGGCTCTTCCT 1353
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                                                                                                                                                                                                                                                                                                                                                             997 TACCAGTGCATGGCAAAGAACGTGGCCGGAGAGGTGAAGACGCGAAGAGGTGACCCTCAGG 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1234 TCTGGCGGGCTTTACATACAGAACGTCGTACAGGGGGACAGCGGAGAGAGTATGCGTGCTCT 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal 142
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                                                                                                                                                                                   105 Val-----AlaValLeuArgGluAspPheGlnIleGlnFroArgAspMetValAlaVal 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 GlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysVal 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluPro 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAspTyrThrGluProValGluLeuLeuAlaValArglleGlnLeuGluAsnValThr 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 erGlyProArgLeuProArgGluAlaArgGluLeuArgGly--------- 270
                                                                                                                                                                                                                                                                                967 ------GAGAGAGAGGATATC 996
                                                                                                                                                                                                                                                                                                                        TyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSer 104
                                       790 CCCCGGATCACCTCCGAGCCCCAGGACGCAGATGTGACCTCGGGGAACACCGTGTACTTC 849
                                                                                                                  850 ACCTGCAGAGCCGAAGGCAACCCCAAGCCTGAGATCATCTGGCTGCGAAACAATAATGAG 909
                                                                                                                                                          LeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuLeu 64
                                                                                                                                                                                                                                         65 GlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyVal 84
                                                                               SerCysArgAlaSerGlyGlnProProProThrileArgTrpLeuLeuAsnGlyGlnPro 44
ProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyProAlaArgMet 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1618 AGAGTCACCCCAGTGTTTGCCAGCATTCCCAGCGACACAAACAGTGGA 1664
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212-869-8864/9741

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unknown

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---GAGATCATCATGCGAAGCTCACC-----GTCCTGCGAGAGGAC---CAGCTG 1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 ThralaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 114
                                                                                                                                                                                                                                                                                                                                           920 GAAGAGCCACCAGATTTATCAGAGCCCCAAGGATCAGATTGGTGTCAGGAGGCGTG 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
                                                                                                                                                                                                                                                                                                    2 AspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 AlaLeuSerThr ---- AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp-
                                                                                                                                                                                                                                                          US-10-047-021-86_COPY_28_303 (1-276) x US-08-447-464-2 (1-5690)
                                                                                                                                                Conservative:
Mismatches:
Indels:
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                                                                                                         Length:
Matches:
                                                                                                            7.98e-09
                                                                                                                       218.50
47.93%
30.88%
14.81%
                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
, NAME/KEY:
, LOCATION:
US-08-447-464-2
                                                                                     Alignment Scores:
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Sequence 2, Application US/08447464
Patent No. 5840842
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHAIASE-SIGMA

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1223 CCTCCTGGCTTCCCCAACATTGACATGGGCCCCCAGTTGAAGGTTGTAGAGCGCACACGC 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 ThralaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 114
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                                                                                                                                                                                                                                                                                                 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
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                                                                                                                                                                                                                                2 AspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
                                                                                                                                                                                                                                                                                                                                                                      22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp-----
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Patent No. 6500318
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-047-021-86_COPY_28_303 (1-276) x US-08-716-679-2 (1-5690)
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      Conservative:
                                  Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Deafface
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1283 ACAGCCACCATGCTTGTGCTGCCAGC---GGAAACCCTGACCCTGAGTTCACTGGTTC 1339
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| AAGACTTCCTGCCTGTGGACCCCAGTGCCAGCAATGGGCGGATCAAGCAGCTTCGGTCA 1399
                                                                                                                                                                 -----ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145
                                                                                                                                                                                                                                                                                                    LysAspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGly 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRECT IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PILING DATE: US/08/716 CTARGET OF CLASCITICATION NUMBER: US/08/716 CTARGET OF 
                                  115 GlnProArgAspMetValAlaValValGlyGluGlnPhe-
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Matches:
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1155 Avenue of the Americas
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schlessinger, Joseph APPLICANT: Yan, Hai TITLE OF INVENTION: NOVEL RECEPTO TITLE OF INVENTION: PHOSPHOTYROSII NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: 2000 ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Amer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08716679
Patent No. 5846800
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TELEPAX: 212-790-9090
TELEPX: 212-869-8864/9741
TELEPX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 base pairs
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TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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218.50
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 18,8
REFERENCE/DOCKET NUMBER:
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STATE: New York
COUNTRY: U.S.A.
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Pred. No.:
Score:
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LOCATION:
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593 GCCCTGCAGATTGAAAGCAGTGAGGAAAACCGACCAGGGCAAATATGAGTGTGTGGCCACC 652
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727 CATCCTGCCCATGAGCCACGGGATCATGCCAGGGGGCAACGTGAACATCA-CCTGCGTGG 785
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                                                                                                                                                                                                                     TyrThrGluProValGluLeuLeuAlaValArglleGlnLeuGluAsnValThrLeuLeu 223
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                                                                                                            AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp
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APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
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83
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
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Matches:
Conservative:
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126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 ---SerGlyProArgLeuProArg 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08348006B Patent No. 5658756
                                                                                                                                                                  653 AACAGCGCCGGCGTGCGC----
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IELECOMMUNICATION INFORMATION
TELEPHONE: 908-594-3905
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206.50
42.36%
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK H
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Percent Similarity:
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Pred. No.:
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Matches:
Conservative:
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CURRENT APPLICATION DATA: US/09/016,434
                                                                                                                                                                                AFLICATION NOMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
LELEPAX: (650) 845-055
INFORMATION FOR SEQ ID NO: 1132: SEQUENCE CHARACTERISTICS: LENGTH: 4078 Base pairs TYPE: nucleic acid STRANDEDNES: single TYPE: STRANDEDNES: single TYPE: INMEDIATE SOURCE: LENGTHERENCE: L
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42.36%
28.82%
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                                                                               HEREWITH
                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; CLONE: 91407624
US-09-016-434-1132
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                230 GGCAAGAAGGTCAACTCTCAGCGCTTTGAGACGATTGAGTTTGATGAG---
                                                         US-10-047-021-86_COPY_28_303 (1-276) x US-08-348-006B-6 (1-6000)
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APPLICANT: RODAN, GIDEON A. APPLICANT: SCHMIDT, AZRIEL
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Local Similarity: 28.82% Match: 14.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 AlaArgMetSerCygArgAlaSerGlyGlnProProProThrIleArgTrp-----
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    CDNA ENCODING A NOVEL HUMAN PROTEIN TYROSINE PHOSPHATASE
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83
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74
                                                                                                                                                                                          ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
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Matches:
Conservative:
Mismatches:
                                                                                       ADDRESSEE: J. MARK HAND - MERCK & CO., INC
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
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206.50
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LENGTH: 6000 base pairs
TYPE: nucleic acid
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TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: (
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                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK H
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                  CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
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---SerGlyProArgLeuProArg 263
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                     Alignment Scores:
Pred. No.:
                                                         US-09-158-657-6
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                                 SerieuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
                                                                                                                                                TyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAenValThrLeuLeu 223
                                                                                                                                                                                                                                                                         TACTCCTCACCTGCCAACCTCTAC---GTGCGAGTCCGCCG-CGTGGCCCCGCGCTTCTC 726
                                                                                                                                                                                                                                                                                                                                                                                      ---GCTCGCCCATGCCATACG 809
                 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLys 146
                                                                      AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
                                                                                                                                                                                      AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09158657
Patent No. 6214564
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUDINIANI COUNTING COUNTING COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: J. MARK HAND - MERCK & CO., INC
126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                               257 ---SerGlyProArgLeuProArg 263
                                                                                                                                                                                                                                                                                                                                                                                                                                            810 TGAAGTGGATGCAGGGGGCCCGAGG 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/158,657 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18992DA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILLING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       ---CCGTGG----
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REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                                                                                                                                                                                                           AACAGCGCCGGCGTGCGC
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: RAHWAY
STATE: NEW JEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLys 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
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                                                 Conservative:
Mismatches:
Indels:
       Length:
Matches:
       63e-08
                     206.50
42.36%
28.82%
14.00%
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APPLICANT: Cunningham, Bruce A. APPLICANT: Cunningham, Bruce A. APPLICANT: Cunningham, Bruce A. APPLICANT: Cunningham, Bruce A. APPLICANT: Crossin, Kathryn L. TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF ADDRESSES: The Scripps Research Institute STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                             95 ThralaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
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727 CATCCTGCCCATGAGCCACGAGATCATGCCAGGGGGAACGTGAACATCA-CCTGCGTGG 785
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                                                                                                                                                   365 ---GAGATCACAGTCCATGCCAAGCTTACT-----GTCCTCGAGAGGACCAGCTGCCC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
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278 AGTGCAGGGCAGTGCTGAGGATCCAGCCG--
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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CITY: La Jolla
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230 GGCAAGAAGGTCAACTCTCAGCGCTTTGAGACGATTGAGTTTGATGAG------ 277
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                                                                                         Sequence 6, Application PC/TUS9410166

Sequence 6, Application PC/TUS9410166

GENERAL INPORMATION:
APPLICANT: RCHALDT, AZRIEL
APPLICANT: RTYLEDGE, SU JANE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
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                    810 TGAAGTGGATGCAGGGGGCCGAGG 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 18992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEPRAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 13825
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.63e-08.
206.50
42.36%
28.82%
14.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                              07065
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Pred. No.:
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203 AspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeu 222
                                                                                         -----CGGGTCAAGGCCACCAAC---AGCATG 716
                                                                                                                                 223 LeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal-----Trp-Leu* 240
                                                                                                                                                                                                                        -- 247
                                                                                                                                                                                                                                                              777 CAGGGCAGCCATTGGTCCTGGAGTGCATCGCCGAGGGCTTTCCCACGCCCACCATCAAA 836
                                                                                                                                                                                                                                                                                                                                 -CACGCCCACTTCCCAGGCACCAGGACCATCATTCAGAAG----- 677
                                                                                                                                                                                                                                                                                                                                                                                                                    717 ATTGACAGGAAGCCGCCCCCCCCCCCCACCAACTCCAGCAGCCACCTGGTGGCCTTG
                                                                                                                                                                                                                                                                                                         -----ArgLeuProAsnLeuThrArgProCysSerGlyPro------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bredeen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Campbell & Flores LLP STREET: Campbell & Flores LLP STREET: A370 La Jolla Village Drive, Suite 700 STATE: California COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carbryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    240 **TrpLysValSerGlyPro***--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/09041886; Patent No. 6235872; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                           260 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 luleuargelyeln 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.81e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..4342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-09-041-886-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::|||
225 GATGTGTC-----CACTTCAAACCCAAGGAAGAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------càcrcrèscreace 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 GluAspPheGlnIleGlnProArgAspMetValAlaValVal-------GlyGlu 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GlnPheThrieuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 ATCACGGGCAACAACAGCAACTTTGCTCAGAGGTTCCAGGGCATCTACCGCTGCTTTGCC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AGCAATAAGCTGGGCACCCCATGTCCCGATCCGGCTC------ATGGCC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 TCAGTGGTTCTGCCTTGCAACCCTCCC---CCAAGTGCAGAGCCTCTCCGGATCTACTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 ATGAACAGCAAGATCTTGCACATCAAGCAGGACGAGCGGTGACGACGGCCAGAACGGC 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 SerieuleuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCysValAla 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerileGinGluProGln 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-047-021-86_COPY_28_303 (1-276) x US-08-506-296B-13 (1-3888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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                 NAME: Fitting, Thomas
REGISTATION NUMBER: 34,163
REFERENCE/DOCKET TSRI
TELECOMMUNICATION INFORMATION:
TELEFAN: (619) 554-2937
TELEFAN: (619) 554-2937
TELEFAN: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHELICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.49e-08
206.00
37.42%
26.69%
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1063 ---TCTGGAAAGCCTGTGCCCACTGTG-----AATTGGATGAAGAATGGAGATGTGGTC 1113
                                                                                                                                                                                                                   535 GACCTGACTCCCAGGTGACTCCCGAGTGGTGGTTTGCCCTCTGGAGCATTGCAG 594
                                                                                                                                                                                                                                                                                                                                                 113 GlnIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGly 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 CTGCAAAGACCATCCAATGTAGTAGCCATTGAAGGAAAAAATGCTGTCCTGGAATGTTGT 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 ProProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 LysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904 GATGATGACAGTGGAATGTATACCTGTGTTGTCACATATAAAAATGAGAATATTAGTGCC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 Ala------ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228
                                                                                                                                                               475 CTCAAGTGTGAAGTCATTGGGGAGCCCATGCCAACAATCCACTGGCAGAAGAAGAACCAACAA 534
                                                                                                                             24 MetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeuAsnGlyGln 43
                                                                                                                                                                                              44 ProleuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62
                                                                                                                                                                                                                                                                                                                                AspleuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 GluGlyProlysProArgProAlaValTrpLeu***TrpLysValSerGlyPro***Arg
                                                                                                                                                                                                                                                                 63 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9405277
GENERAL INFORMATION:
APPLICANT: Bruskin, Arthur
APPLICANT: Jarosz, David B.
APPLICANT: Johnson, Karen
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Tabecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-047-021-86_COPY_28_303 (1-276) x US-09-041-886-24 (1-4608)
 68
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97
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             Conservative:
Mismatches:
Indels:
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 Matches:
                                                                  Gaps:
206.00
42.80%
27.98%
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               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 GlnIleGlnDroArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 ProLeuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 MetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeuAsnGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAlaArgLeuSerValAlaValLeuArgGluAsp------------------------
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68
36
97
42
                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
ADDRESSEE: Banner, Birch, McKie & Beckett
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Matches:
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                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05277
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                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: ASATA A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 0107
TELECOMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.929
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID
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42.80$
27.98$
13.97$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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                                 Washington
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Query Match:
                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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PCT-US94-05277-1
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1030 GGCTCTGTGGAAGGGCCGGGGCTGGAAACCCTAGC-CCTGACCCTGGGGATCCTGGGAGG 1088
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                                                                                                                                                                                                                                                                                                                                                                        CCC---GCCCAGCCCCCACCTCAAATCCACTGGATCAAGGATGGCAGGCCCCTGCCCTT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGlu***ThrTyrMetCysValAlaThrAsn---SerAlaGlyHisArgGluSerArg 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 ValArgileGinLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 ArgProCysSerGlyProArgLeuProArgGlu-----AlaArgGluLeuArgGlyGln 271
                                                                                                                                      ATGGTGACCCCAGCTCGGGGAGGACTCTCCACCCCTTCTCCTGTAGCTTCACCCCT 642
                                                                                                                                                                                                                         GGCCTTCCCCGGCGCCCGAGCCCTGCACACGGCCCCCATCCAGCTCAGGGTCTGGAGTGAG 702
                                                                                                                                                                                                                                                               -----SerArgGlyAlaArgLeuSerValAlaValLeuArgGlu---AspPheGln 113
                                                                                                                                                                                                                                                                                                       103 CACCGAGGIGGGGAGGGCCCAACGIGGACGCIGIGCCACTGAAGGAAGTCCAGIIGGIG 762
                                                                                                                                                                                                                                                                                                                                               IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 133
                                                                                                                                                                                                                                                                                                                                                                                                                             ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAGGAAGAGACCCAAAGACACCAAAGACTTTTCACGCTCCATTCGGAGCTG
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                                                                                                 GlyVal----TyrThrCysGluAlaSer---
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                  LeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThrAspLeu
                                                                                                                                                                               ------AsnArgLeuGlyThrAlaVal------
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Nucleotide Sequence of LICAM and
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Characterized Thereby
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
TITLE OF INVENTION: A Method for Ch
TITLE OF INVENTION: Nucleotide Sequence of TITLE OF INVENTION: THE OF INVENTION: THE Nucleotide Sequence of TITLE OF INVENTION: Characterized T
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GENERAL INFORMATION:
APPLICANT: Scherid, Ann Marie
APPLICANT: Scherid, Ann Marie
APPLICANT: Scherid, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION EMPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
TITLE OF INVENTION: USES THEREOF
FILE REPRENENCE: 0575/62175
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SC. 10
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                                                                                                                                                                                                                                                                                192 ArgalaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 211
                                                                                                                                                                                                                                                                                                                                                                  Ala------ValArgileGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 GluGlyProLysProArgProAlaValTrpLeu***TrpLysValSerGlyPro***Arg 248
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                                                                              787 GTTTCT---GGCTATCCTCCACCAAGTTTTACCTGGTTACGAGGCGAGGAAGTCATCCAA 843
                                                                                                                      LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171
                                                                                                                                               CTGCAAAGACCATCCAATGTAGTAGCCATTGAAGGAAAAGATGCTGTCCTGGAATGTTGT 786
                                        ProProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 152
                                                                                                                                                                                                      LysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6563015
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1114 ATTCCTAGT 1122
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US-09-638-649-2
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Best Local Similarity:
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SEQ ID NO 2
LENGTH: 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202
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                    --CACTTCAAACCCAAGGAAGAG 269
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                                                                                                                                                                        315 ATCACGGGCAACAACAGCAACTTTGCTCAGAGGTTCCAGGGCATCTACCGCTGCTTTGCC 374
                                                                                                                                  83
                                                      61 Leu-----LeuLeuLeuGinProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78
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                                                                                                                                  -----LeuGlyValTyrThrCysGluAla
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TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
                                                                                            270 creserstascestarcairesceic
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; Patent No. 5872225
; GENERAL INFORMATION:
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240 GATGGTGTC--
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US-08-341-843B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: C. PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing of
TITLE: human ilCAM: an interspecies comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1042
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Matches:
Conservative:
Mismatches:
Indels:
                                                                    ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -26 to 1016
                                                                                                                                                                                                                                                               CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: MINIACh, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELEPHONE: (216) 861-582
TELEPHONE: (216) 861-582
TELEPAS: (216) 980162
INFORMATION FOR SEQ ID NO: 6:
LENGTH: 1942
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INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene CDNA Library 9362
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TOPOLOGY: linear
MOLECULE TYPE: nucleic acids
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36.59%
26.83%
13.42%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
        CITY:
SIATE: Ohio
COUNTRY: U.S.A.
TTP: 44114-2518
  Suite 700
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Query Match:
DB:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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706 ATTGACAGGAAGCCGCCCTCTTCCCCACCAACTCCAGCACCTCGTGGCCTTG 765
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349 AGCAATBAAGCTGGGCACCGCCATGTCCCATGAGATCCGGCTC------ATGGCC 396
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                                                                                                                                                                                                                                                                                                                                                                        126 GlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LysAspGlyLysProteuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCysValAla 182
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-----AGCCTCAAGTGTGAGGCCAGTGGCAAGCCCGAAGTGCAGTTCCGCTGGACGAGG 213
                                                                            -----CACTTCAAACCCAAGGAAGAG 243
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                                                                                                                  Leu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78
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                                      41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
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A Method for Characterizing the
Nucleotide Sequence of L1CAM and
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Characterized Thereby
                                                                            214 GATGGTGTC------
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; Patent No. 5969124
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TITLE OF INVENTION:
PATENT NO. 5969124
TITLE OF INVENTION:
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APPLICANT: Lemmon
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: Molecular structure and functional IIILE: testing of human LICAM: an IIILE: interspecies comparison.
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,843B
FILING DATE: No. 5872225ember 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                ZIP: 44114-2518
COMMUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: Stratagene cDNA Library 936206
CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-18 week fetus
                                                                                                                                                                                            COMPUTER: Compaq Prolinea 5100e OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO:
                STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ADDRESSEE: Minnich & McKee
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198.00
36.59%
26.83%
13.42%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: irrelevant
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ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17
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STRANDEDNESS: sing
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                                                                                                RY: U.S.A.
44114-2518
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Best Local Similarity:
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1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/427,497E
FILING DATE: April 24, 1995
CLASSIFICATION: 435
FRIOR APPLICATION DATA: APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional
TITLE: testing of human LICAM: an
TITLE: interspecies comparison.
JOURNAL: GENOMICS
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                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
                                                                                                                                                                                                               셮
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
STATE: Ohio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: Stratagene cDNA Library 936206 CLONE: synthesis of 4 clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: nucleic a HYPOTHETICAL: irrelevant ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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                                                                                    -----CACTTCAAACCCAAGGAAGAG 243
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ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThr1leArgTrpLeuLeu
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Job time : 74.5389 secs
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US-10-047-021-31
US-10-411-24-31
US-09-978-637-210
US-09-978-637-210
US-09-978-192A-210
US-09-98-192A-210
US-09-98-192A-210
US-09-98-193A-210
US-10-143-034A-210
US-10-145-017A-210
US-10-145-017A-210
US-10-165-057A-210
US-10-165-247A-210
US-10-165-247A-210
US-10-165-247A-210
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PZ016P2
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CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/262,066
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 1090-10-4
PRIOR PLILING DATE: 1999-03-04
PRIOR PLILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-05
PRIOR PILING DATE: 1997-09-05
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Publication No. US20040002591A1
GENERAL INFORMATION:
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       Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=Cqg12_1/USPFO spool p/USIO047021/runat_30012004_145455_24678/app_query.fasta_1.910
-Q=/Cqg12_1/USPFO spool p/USIO047021/runat_30012004_145455_24678/app_query.fasta_1.910
-DB=PublIshed Applications NA -OFWI=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NGRM=ext -HRAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10047021_@CGN 1 1 129 @runat_30012004_145455_24678
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG $GORES=0 -WAIT -DSPBLOCK=100
-NCPU=6 -ICPU=3 -NO WMAP -ILARGEQUERY -NEG $GORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBV TIMEOŪT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
                                                                                                                  January 31, 2004, 14:37:41; Search time 303.648 Seconds (without alignments) 3312.713 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| Cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                       - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
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CURRENT APPLICATION NUMBER: US/10/411,224
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/722,329
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/057,663
PRIOR PILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,973
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US-10-411-224-31
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                   PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,666
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 206
SOFWARE: PATCHIN VET: 2.0
  APPLICATION NUMBER: US 60/058,667
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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 Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                           Paoni, Nicholas P.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
                                                      Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                 Pan, James
                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly
                                                                                                                                               AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
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APPLICANT: Baker Kevin P.
APPLICANT: Bacstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eacon, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Frivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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R APPLICATION NUMBER: 60/080333

R FILING DATE: 1998-04-01

R PELLING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080334

R APPLICATION NUMBER: 60/081070

R APPLICATION NUMBER: 60/081070

R APPLICATION NUMBER: 60/081049

R FILING DATE: 1998-04-08

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R APPLICATION NUMBER: 60/081195

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R FILING DATE: 1998-04-09
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081817
R FILING DATE: 1998-04-15
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R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/08204

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R APPLICATION NUMBER: 60/08204

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R PILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/08332

R FILING DATE: 1998-04-23

R APPLICATION NUMBER: 60/08332

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R APPLICATION NUMBER: 60/083495

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083495

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R APPLICATION NUMBER: 60/083495

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                                                     R APPLICATION NUMBER: 60/080194
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
R FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/084366
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1998-05-05 NUMBER: 60/084414 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-07 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-13 1998-05-15	larity: 98-53* imilarity: 98.17* 97.08* 10.:	1 GlnaspSerProProGlnileLeuValHisProGlnAspGlnLeuPheGlnGly 	21 ProhlaargwetsercysargalaserGlyGlnProProProThrIleArgTrpLeuLeu 	41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyTh:	61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 	81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGl) 	101. AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnFroArgAspMetVal
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R FILING DATE: 1997-10-17
R APPLICATION NUMBER: 60/064249
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R APPLICATION NUMBER: 60/065311
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R APPLICATION NUMBER: 60/066364
R FILING DATE: 1997-11-13
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R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
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R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/079923
R FILING DATE: 1998-03-30
R APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
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FILING DATE: 1998-03-11
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/081049
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/080328
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373 GCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTG 432
                                                                                                                                     433 GCTGTGGTGGGCGGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGGCCC 492
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APPLICANT: Wood, William I.
IITLE OF INVENTION: Secreted and Transmembran
FILLE OF PROFILE OF ACIDS Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/978,697
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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PRIOR FILING DATE: 2001-07-30
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Gerber, Hanspeter
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Goddard, Audrey
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10. Sophia S.
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Desnoyers, Luc
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Pan, James;
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R APPLICATION UNDERS: 60/084639
R FILING DATE: 1998-05-07
R APPLICATION WINDER: 60/084640
R FILING DATE: 1998-05-07
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R APPLICATION NUMBER: 60/084508
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                              FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/082700
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G DATE: 1998-04-28
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APPLICATION UNDERS: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
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                CATION NUMBER: 60/081955
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ICATION NUMBER: 60/083499
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PRIOR APPLICATION NUMBER: 60/085323 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/08582 PRIOR APPLICATION NUMBER: 60/085700 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085689 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085689 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085579 PRIOR FILING DATE: 1998-05-15 PRIOR PLILNG DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/08550 PRIOR APPLICATION NUMBER: 60/08550 PRIOR FILING DATE: 1998-05-15 PRIOR FILING DATE: 1998-05-15 PRIOR PLILNG DATE: 1998-05-15 PRIOR FILING DATE: 1998-05-15 PRIOR PLILNG DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085704 PRIOR FILING DATE: 1998-05-15	Alignment Scores: 2.72e-127 Length: 3716 Score: 1432.00 Matches: 268 Score: 98.53\$ Conservative: 1 Best Local Similarity: 98.17\$ Mismatches: 3 Query Match: 10 Gaps: 0	-86_COPY_28_303 (1-276) x US-09-978-697-210 (1-3716)	<pre>1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20</pre>	21 ProAlaArgWetSerCysArgalaSerGlyGlnProProProThrIleArgTrpLeuLeu 40	41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60	61 LeuLeuLeuLeuGInProProAlaArgGIyHisAlaHisAspGIyGInAlaLeuSerThr 80 	81 AspleuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100 	101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120	121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140 	141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160	ACAGTETCATGGTGGAAAGATGGGAAACEEETGGGEETCCAGECCGGAAGGEACACAGTG 55.	161 SerGlyGlySerLeuLeuMetAlaargAlaGluLy8SerAspGlu***ThrTyrMetCys 180	181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200 	1 ProGlamspTyrThrGluBroValGluLeuLeuAlaValArglleGlaLeuGluAsnVal 22	673 CCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 732	221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/082797
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       FILING DATE: 1998-03-20
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PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
LE REFERENCE: P2630P1C9
                                                                                                                                                                            260 gieuProArgGluAlaArgGluLeuArgGlyGlnArg 272
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CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                  RESULT 5
US-09-978-192A-210
; Sequence 210, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Abhkenazi, Avi
; APPLICANT: Baker Kevin P.
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PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR PILING DATE: 1997-11-03

PRIOR PILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-20

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-11

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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E
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Pan, James:
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Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Bater Kevin P.
APPLICANT: Baten, David
APPLICANT: Eaton, Dan
APPLICANT: Faton, Dan
APPLICANT: Filvaroff, Napoleon
APPLICANT: Filvaroff, Ellen
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Mismatches:
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R FILING DATE: 1998-05-07

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-07

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084600

R PILING DATE: 1998-05-07

R PILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084643

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

R PILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
                                FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
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FILING DATE: 1998-05-07
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Percent Similarity:
Best Local Similarity:
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                                                          PRINCH PR
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R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R APPLICATION NUMBER: 60/080327

R APPLICATION NUMBER: 60/080327

R APPLICATION NUMBER: 60/080327

R APPLICATION NUMBER: 60/080328

R APPLICATION NUMBER: 60/080338

R APPLICATION NUMBER: 60/080333

R APPLICATION DATE: 1998-04-01
                                                    FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080165
                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
                                                                                                                                                                                                                                                                                                                                                                                       APPLING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-15
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082796
1LING DATE: 1998-04-23
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FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083499
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PPLICATION NUMBER: 60/083558
 NUMBER: 60/080105
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PPLICATION NUMBER: 60/082797
                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081071
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                     998-03-3
PPLICANT: Wood, William I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P2630P1C63
CHRENT APPLICATION NUMBER: US/09/999, 832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILLING DATE: 2001-07-30
PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-11-13
PRIOR FILLING DATE: 1997-11-13
PRIOR FILLING DATE: 1997-11-13
PRIOR FILLING DATE: 1997-11-21
PRIOR PELLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07763
PRIOR FILLING DATE: 1998-03-10
PRIOR FILLING DATE: 1998-03-11
PRIOR PELLING DATE: 1998-03-12
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-03-26
                                                                               Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
                                                                                                                                                                                                                                                                                                                 Tumas, Daniel
Williams, P. Mickey
                                                                                                                                                                                                                                                       Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                   Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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                                                                                                                                                                                                                                         Paoni, Nicholas
                                                                                                                                                    Hillan, Kenneth
                                                                                                                                                                     Ivar J
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APPLICANT:
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313 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC 372
                                                                                                                                                                                                                                                                                                                                                                                                            552
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                                                                                                                                                                                                    121 AlavalValGlyGluGlnPheThrLeuGluCysGlyProProfrpGlyHisProGluPro
                                                                                                                                                                                                                                          433 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                493 ACAGICTCAIGGIGGAAAGAIGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 CCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAAATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal
                                                                  101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal
                                                                                                                                     373 GCTCGGCTGTCTGTGGCTGTCCTCCGGGATTTCCAGATCCAGCCTCGGGACATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys
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                                                                                                                                                                                                                                                                                                                                         ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                        R APPLICATION NUMBER: 60/083742

R FILING DATE: 1998-04-30

R FILING DATE: 1998-05-05

R APPLICATION NUMBER: 60/084414

R APPLICATION NUMBER: 60/084414

R PILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/08441

R FILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084637

R FILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084637

R FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-05-07
APPLICATION UNMBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: 60/085704
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FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 CATION NUMBER: 60/083545 IG DATE: 1998-04-29 FILING DATE: 1998-04-30 APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 CATION NUMBER: 60/082700 CATION NUMBER: 60/083554 G DATE: 1998-04-29 CATION NUMBER: 60/083558 IG DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 APPLICATION NUMBER: 60/083742 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06 PPLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/082804 APPLICATION NUMBER: 60/082797 CATION NUMBER: 60/083336 APPLICATION NUMBER: 60/083392 APPLICATION NUMBER: 60/083559 CATION NUMBER: 60/084637 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 998-04-27 PRESENTED BY STREET BY STR

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 210, Application US/09978608A; Publication No. US20030045462A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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SEQ ID NO 210
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                  PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08538
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-15
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PRIOR PRILING DATE: 1998-05-15
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APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Kuo, Sophia S.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, Wood, Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, Wood
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Hillan, Kenneth
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US-09-978-585A-210
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                      ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu
                                                                                                                                          AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Betstein, David
APPLICANT: Beton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Audrey
APPLICANT: Grimaldi, J. Chrigh
APPLICANT: Grimaldi, J. Chrith
APPLICANT: Grimaldi, J. Chrith
APPLICANT: Grimaldi, J. Chrith
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R FILING DATE: 1998-03-20
R PAPLICATION NUMBER: 60/078936
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R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
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FILING DATE: 1998-04-08
APPLICATION DATE: 1998-04-0
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILLING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/081819
                                       APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081952
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CATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/081071
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                                           ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
                                                                                                                                   ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
                                                                         733 ACACTGCAACCCCGGATCCTGCAGAGGCCCCCAAGCCTAGACCGGCGGTGTGGGCTCAGC 792
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                 260 gleuProArgGluAlaArgGluLeuArgGlyGlnArg 272
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CURRENT FILING DATE: 2001-10-15
PRIOR PELICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/018585
PRIOR APPLICATION NUMBER: 60/06220
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
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Grimaldi, J. Christopher
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Hillan, Kenneth
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Botstein, David
Desnoyers, Luc
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Tumas, Daniel
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R FILING DATE: 1998-05-05
R APPLICATION NUMBER: 60/084414
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R APPLICATION NUMBER: 60/084637
R APPLICATION NUMBER: 60/084640
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R APPLICATION NUMBER: 60/08336

R FLING DATE: 1998-04-27

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R APPLICATION NUMBER: 60/08332

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R APPLICATION NUMBER: 60/083495

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APPLICATION UNMBER: 60/082797
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APPLICATION NUMBER: 60/082796
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FILING DATE: 1998-05-07
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	s e	73 CAGGACTCC	CCGCCCCAGATCCTA	GTCCACCCCAGGACC SerGlvGlnProProP	roThrIleAroTrn[en]en	132
	; සි			TCAGGCCAGCCACCTC	CCGCGGGATGAGCTGCCAAGCCTCAGGCCAGCCACCCACC	, ,
	Š	41 AsnGlyGln		ProProAspProHisH	isLeuLeuProAspGlyThr	9
	qq	193 AATGGGCAG	GCAGCCCCTGAGCATGGTGCCC	CCCCAGACCCACACC	CCAGACCCACCACCTCCTGCCTGATGGGACC	252
	È	61	LeuGlnProProAla	ArgGlyHisAlaHisA	LeuleuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr	80
	g	m	CTACAGCCCCCTGCC	CGGGGACATGCCCACG	ATGCCAGGCCCTGTCCACA	31
	& &		ValTyrThrCysGlu	AlaSerAsnArgLeuG 	AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly	0 7
	8	313 GACCTGGGT	GICTACACATGTGAG	GCCAGCAACCGGCTTG	GCACGCCAGTCAGCAGAGGC	37
	Š	_	SerValAlaValLeu	ArgGluAspPheGlnI 	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	12
	셤	373 GCTCGGCTG	rcrereccrerecte	CGGGAGGATTTCCAGA	TCCAGCCTCGGGACATGGTG	432
-	ć	н	GlyGluGlnPheThr	LeuGluCysGlyProP	AlavalValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro	Н
	qq	433 Gerereie	gercaecaerracr	cresaareresecese	ceresescaeceaeses	492
	č	141 ThrValSer	TrpTrpLysAspGly	LysProteuAlateuG	ThrvalSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal	16
	Ор	493 ACAGTCTCA	regregaaagarege	AAAcccreecceree	Ageceggaagecacacagre	552
	È	161 SerGlyGly	SerLeuLeuMetAla	ArgAlaGluLysSerA	SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys	180
	g g	553 TCCGGGGG	rcccrecreareca	AGAGCAGAGAAGAGTG	ACGAAGGACCTACATGTGT	612
	È	181 ValAlaThr	AsnSerAlaGlyHis	ArgGluSerArgAlaA	ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu	200
	ДQ	613 GreeceAce	AACAGGGCAGGACATI	AGGAGAGCCGCGCAG	cccederriccarccadeae	672
	ò	201 ProGlnAsp	TyrThrGluProVal	GluLeuLeuAlaValA	ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal	220
	qq	673 ccccaddac	racacesaeccrere	saccricrecrerec	GAATTCAGCTGGAAAATGTG	732
	Š	221 ThrLeuLeu	AsnProAspProAla(GluGlyProLysProA	ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu***	240
	qq	733 ACACTGCTG	AACCCGGATCCTGCA	GAGGCCCCAAGCCTA	GACCGGCGGTGTGGCTCAGC	792
	δ	241 TrpLysVal	SerGlyPro***-Arg	gLeuProAsnLeuThr	TrpLysValSerGlyPro***-ArgLeuFroAsnLeuThrArgProCysSerGlyProAr	260
	qa	793 TGGAAGGTC	AGTGGCCTGCTGCG	ccreccaarcrraca	CGGCCTTGTTCAGGACCCAG	852
	λō	260 gLeuProAr	gLeuProArgGluAlaArgGluLeuArgGlyGlnAr	uArgGlyGlnArg 27	2	
	QQ Q	853 ACTGCCCCG	GGAGGCCAGGGAGCT	ccerececadade 88	6	
	RESULT 11 US-09-978 ; Sequence ; Publica	SULT 11 :-09-978-403A-210 Sequence 210, Application US/09 Publication No. US20030050240A1 GENERAL, INFORMATION	97840	3A		
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R FILING DATE: 1998-03-27

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RAPLICATION NUMBER: 60/080328

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RELING DATE: 1998-04-01

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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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PPLICANT: Wood, William I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
ILE REPERENCE: P2630P1C17
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FILE REFRENCENCE: PASA DELLO.

CURRENT PELLING DATE: 2002-03-19

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PRIOR PELLING DATE: 12097-10-17

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PRIOR APPLICATION NUMBER: 60/079656

PRIOR APPLICATION NUMBER: 60/079656

PRIOR PELLING DATE: 1998-03-20

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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/079728
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
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Shelton, David L.
Stewart, Timothy A.
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                     Gerber, Hanspeter
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                                                                        Botstein, David
Desnoyers, Luc
Ashkenazi, Avi
Baker Kevin P
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SerGlyGlySerLeuLeuMetAlaArgAlaGluLy8SerAspGlu***ThrTyrMetCys 180
                                                                                                                                                                                                                                 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
                                                                                                                                                                                                                                                                                                                                           AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
                                                                                                                                                                                                                                                                                                                                                                           ThrValSerTrpTrpLyeAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
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              80
                                                                                                                                                           ACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG
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                                              CTTCTGCTACTACAGCCCCTGCCCGGGGACATGCCCCACGATGGCCAGGCCCTGTCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly
                 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wai-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Shelton, David L.
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Kuo, Sophia S.
Napier, Mary A.
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US-09-978-564A-210
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Matches:
Conservative:
Mismatches:
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR APPLICATION NUMBER: 60/08359
PRIOR APPLICATION NUMBER: 60/08359
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
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PRIOR PILING DATE: 1998-05-05
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PRIOR APPLICATION NUMBER: 60/085339
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08532
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08558
PRIOR PILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/08558
PRIOR PILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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A PELLING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081195

R PLING DATE: 1998-04-08

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R PLING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R PILING DATE: 1998-04-05

R PILING DATE: 1998-04-15

R PILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083322
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-29
                                        FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
           APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-21
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APPLICATION WINDER: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
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FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
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APPLICATION WINBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/083554
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PRIOR
                                                 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
                                                                                                                                                                                    CURRENT FILING DATE: 2001-10-16
PRIOR PILING DATE: 2001-0-16
PRIOR PILING DATE: 2001-0-16
PRIOR PILING DATE: 2001-0-30
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06544
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Goddwaft, Paul J.
APPLICANT: Goddwaft, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kliavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Aun
APPLICANT: Roy, Margaret Aun
APPLICANT: Roy, Margaret Aun
APPLICANT: Roy, Margaret Aun
APPLICANT: Timelhy A.
APPLICANT: Timelhy A.
APPLICANT: William I.
APPLICANT: WILLIAM 
                                                                                                                                                                                                       ThrieuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Desnoyers, Luc
Eaton, Dan
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Matches:
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PRIOR PILING DATE: 1998-05-07
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PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-05-13
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PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
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R APPLICATION NUMBER: 60/079294

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R APPLICATION NUMBER: 60/079656

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R APPLICATION NUMBER: 60/081070
R FILING DATE: 1998-04-08
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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071 FILING DATE: 1998-03-31 APPLICATION UNMBER: 60/080327 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 PLICATION NUMBER: 60/079786 LING DATE: 1998-03-27 PLICAȚION NUMBER: 60/079920 APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/07791 APPLICATION NUMBER: 60/079689 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079728 NG DATE: 1998-03-30 ICATION NUMBER: 60/079923 ICATION NUMBER: 60/080105 WG DATE: 1998-04-01 ICATION NUMBER: 60/080333 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081955 APPLICATION NUMBER: 60/082568 ICATION NUMBER: 60/080334 FILING DATE: 1998-03-30 FILING DATE: 1998-04-01 LING DATE: 1998-03-2 FILING DATE: 1998-04-1 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

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R FILING DATE: 1998-05-13
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R APPLICATION NUMBER: 60/084639

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

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PILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/08441 FILING DATE: 1998-65-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 1998-05-05 1998-05-06

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Matches:
Conservative:
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
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RESULT 14

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R APPLICATION NUMBER: 60/079786

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R APPLICATION NUMBER: 60/081070
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R APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/081955
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PLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/082569
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                                                                                   CTTCTGCTGCTACAGCCCCCTGCCCGGGACATGCCCACGATGGCCAGGCCCTGTCCACA 312
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Gao, Wei-Ciang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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; Sequence 210, Application US/09978824
; Sellication No. US20030055216A1
; GENERAL INFORMATION:
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Ferrara, Napoleon
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Kuo, Sophia S.
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241 TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
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January 30, 2004, 15:52:09; Search time 13.3472 Seconds (without alignments) 1988.631 Million cell updates/sec Run on:

score: Title: Perfect (

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
	Score	Query	Length	DB		Description
	448.5	30.4		7	T14160	transmembrane rece
~	445.5	30.2	_		T30805	. 'dutt1 protein - mo
_	414.5	28.1	134	~	T14316	rig-1
	354.5	24.0			T29549	hypothetical prote
	354.5	24.0	1273	~	T42405	sax-3 protein - Ca
	253	17.2	1535	~	S46224	peroxidasin - frui
_	251	17.0	-	7	S26180	neurofascin - chic
_	245	16.6	_		151669	tumor suppressor -
•	234.5	15.5		7	846216	leukocyte antigen-
10	232.5	15.8	3 1897		TDHULK .	leukoc
_	230.5	15.6		• •	A34695	
~	228	15.5			A49356	transient axonal g
_	228	15.5		•	T20992	hypothetical prote
	228	15.5	5 5198		T43290	hemicentin precurs
	225	15.3		~	S18252	heparan sulfate pr
	222	15.1			A56178	protein-tyrosine-p
_	222	15.]	~		TDPFLK	protein-tyrosine-p
_	220.5	14.9			C54689	protein-tyrosine-p
_	219.5	14.5			A53449	plasmacytoma-assoc
_	219	14.8	-		158164	BIG-1 protein - ra
21	218.5	14.8	_	•	I58148	protein-tyrosine-p
~	218.5	14.8	_		S46217	protein-tyrosine-p
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ı۸	213.5	٠	5 1036		S22383	axonin 1 precursor
	212.5	•	4 1070		JC4593	. protein-tyrosine k
_	209	14.2	2 267		A38442	probable tumor sup
_	208.5	14.1	1262		83	protein-tyrosine-p
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œ	206	205	204.5	203.5	201	195.5	195.5	195	194.5	194.5	192	191.5	191	191	189
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ALIGNMENTS

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transmembrane receptor protein Robol - rat
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
R;Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.;
Cell 92, 205-215, 1998
A;Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam. A;Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam. A;Accession: T14160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A)Residues: 1-1651 «KID>
A)Residues: 1-1651 «KID>
A)CTOSS-references: EMBL:AF041082; NID:92811215; PID:92811216; PIDN:AAC39960.1
A)CTOSS-references: EMBL:AF041082; NID:92811215; PID:92811216; PIDN:AAC39960.1
A)Description: appears to function as the gatekeeper controlling midline crossing C; Keywords: transmembrane protein

Gaps <u>ب</u> Length 1651; Indels Query Match 30.4%; Score 448.5; DB 2; Best Local Similarity 42.2%; Pred. No. 1.9e-26; Matches 92; Conservative 31; Mismatches 86;

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57

64 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP 123 1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP Š 셤

117 |:| |: ||: ||: ||: || || || || || || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: | 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 8 g

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YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215 238 178 ò 셤

RESULT 2 T30805

dutt1 protein - mouse

N.Alternate names: transmembrane receptor protein Robol homolog C;Species: Mus musculus (house mouse) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: T30805 R;Mu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P. R;Mu, M.C.; Mu, M.C.; Rights, P. R;Mu, M.C.; Mu, M.C.; Mu,

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Species: Caenorhabditis elegans
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rig-1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14316
R;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.
B;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.
A;Reference number: 217975
A;Accession: T14316
A;Reference trype: mkDary; translated from GB/EMBL/DDBJ
A;Residues: 1-1344 < YUA.
A;Residues: 1-1344 < YUA.
A;Residues: 1-1344 < YUA.
A;Cross-references: EMBL:AF060570; NID:g4206385; PID:g4206386; PIDN:AAD11628.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGTLLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SGALFF---PRIVH---GRRSRPDEGVYTCVARNYLGAAASRNASLEVAVLRDDFRQSPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMCVATNSAGHRESRAAR-VSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAE----- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|: |: |: | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | | : | : | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | | : | : | | : | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1612 <WUM>
A;Residues: 1-1612 <WUM>
A;Cross-references: EMBL: X17793; NID:e1329712; PID:e1329713; PIDN:CAA76850.1
A;Experimental source: brain
C;Genetics:
A;Gene: duttl
A;Map position: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ODSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDP--HH-LLLP
                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 1612;
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                                                                                                                                                                                                                                                                                                                                                                                                                         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                                                                                             87;
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T29549
hypothetičal protein ZK377.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                              30.2%; Score 445.5; DB 2
llarity 41.7%; Pred. No. 3.2e-26;
Conservative 31; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 GPKPRPAVWLXWK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPOPN----LHWR 270
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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Rizallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp. A;Accession: T42405
A;Accession: T42405
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1273 <ZAL>
A;Cross-references: EMBb:AF041053; NID:g2804779; PIDN:AAC38848.1; PID:g2804780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 41; Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQP-GRHTV-SGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 YQCVANNMVGERVSNPARLSVFEKPKFEQEPKDMT------VDVGAAVLFDCRVTGD 252
                                                                                                                                                                                                                                                                      A;Residues: 1-423 <NHA>
A;Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3
A;Experimental source: strain Bristol N2; clone ZK377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sax.3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWYKDGQPVITNKEQVNSHRIVLDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWYKDGQPVITNKEQVNSHRIVLDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POILVHPODOLFQGPGPARMSCRASGQPPPT--IRWLLNGQPL--SMVPPDPHHLLPD-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PQILVHPQDQLFQGPGPARMSCRASGQPPPT--IRWLLNGQPL--SMVPPDPHHLLPD-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
24.0%; Score 354.5; DB 2; Length
Best Local Similarity 34.0%; Pred. No. 7.2e-20;
Matches 96; Conservative 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 PKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiAccession: T29549
Ribhan, M.; Hawkins, J.
Submitted to the EMBL Data Library, February 1997
A; Description: The sequence of C. elegans cosmid ZK377.
A; Reference number: Z20639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 24.0%; Score 354.5; DB 2; 1 Similarity 34.0%; Pred. No. 2.4e-19; 96; Conservative 44; Mismatches 101;
                                                                                                                                                                               A;Accession: T29549
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: X
A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3
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A;Cross-references: EMBL:X65224; NID:g63659; PIDN:CAA46330.1; PID:g63660
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i
F;279-336/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor suppressor - African clawed frog
C.Species: Xenopus laavis (African clawed frog)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C.Accession: I51669
R.Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R. Dev. Biol. 166, 654-665, 1994
A.Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the A.Accession: I51669
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                                                                                                                                                                                                                                                   413
                                                                                                                                                                                                                                                                                                                                 414 -------RDTQIGSS--AVYQCNASNEHGYLL---ANAFVSVL----DVPPRILAPRN 455
                                                                                                                                                                                                                                                                                                                                                                                                  118 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 175
                                                                                                                                                                                                                                                                                                                                                                                                                              207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 S-GYPTPTIVWMQGDEPVPIRTRKYSVLGGSNLLISNVTDDDAGAYTCVATYKNENTSFS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 ADLTVMVPPQFLNHPANLYAYESMDIEFE-----CAVSGKPSPTV--KWTKNGEVVI 372
                                                                                                                                                                                                     63
                                                                                                                                                                                                                               64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 DLGVYTCEASNRLGTAVSRGARLSVAVLRED-----FQIQPRDMVAVVGEQFTLECGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 --GVYRCLAKNPGSARVGNEAEL--RILSĘSGLHRQQVFLQRPSNVVAIEGQDAVLECAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ARMSCRASGOPPPTIRWLLNGQPLSMVPPDPHHL-LPDGTLLLLQPPARGHAHDGQALST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARVSIQEPODYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRL
                                                                                                                                                                                                     5 PQILVHPQDQLFQGPG-PARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1427 <PIE>
A;Cross-references: EMBL:U10986; NID:g606873; PIDN:AAA70168.1; PID:g606874
C;Genetics:
                                                                                                                                                      Gaps
                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 245; DB 2; Length 1427; 31.0%; Pred. No. 7.1e-11; tive 32; Mismatches 99; Indels 3
                                                                                                     Length 1272;
                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte antigen-related protein precursor - rat
N;Alternate names: leukocyte common antigen homolog
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
                                                                                                  17.0%; Score 251; DB 2;
34.5%; Pred. No. 2.2e-11;
vative 34; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ||||| | |:: |: :::|
515 GIYTCVATNILGKVEAQ-VRLEVKOP 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 XTYMCVATNSAGHRESRAARVSIQEP 201
                                                                           Query Match
Best Local Similarity 34....
Best Local Similarity 34....
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nes 75; Conserv
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PS 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: XDCCa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
846224
percaidasin - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
C;Accession: $46224
R;Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke
EMBO J. 13, 3438-3447, 1994
A;Title: Percaidasin: a novel enzyme-matrix protein of Drosophila development.
A;Reference number: $46224
A;Accession: $46224
A;Accession: $46224
A;Accession: $46224
A;Residues: 1-1535 vNEL-
A;Residues: 1-1535 vNEL-
A;Cross-references: GB:U11052; NID:G531384; PIDN:AAA61568.1; PID:G531385
C;Superfamily: percaidasin; myeloperoxidase homology; proteoglycan amino-terminal homology cPAH4>
F;661-1350/Domain: myeloperoxidase homology <PAH4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurofascin - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26180
R;Volkmer, H.; Hassel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
A;Cell Biol. 118, 149-161, 1992
A;Title: Structure of the axonal surface recognition molecule neurofascin and its relating A;Reference number: S26180; MUID:92317154; PMID:11377696
A;Accession: S26180
A;Accession: S26180
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1272 <VOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         icross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385; Superfamily: peroxidasin; myeloperoxidase homology; proteoglycan amino-terminal homology; PAH4>
19-44/Domain: proteoglycan amino-terminal homology <PAH4>
161-1350/Domain: myeloperoxidase homology <MPX>
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|LILLQP------NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTAPQSQT 472
SLFLLKVNSGKNGKD----SDAGAYYCVASNEHGEVKSNEGSLKLAMLREDFRVRPRTV 142
                                                                             YMCVATNSAGHRESRAARVSI-----QEPQDYTEPVELLAVRIQLENVTLLNPDPAEG 230
                                                                                                                                                                                203 YQCVANNMVGERVSNPARLSVPEKPKFEQEPKDMT------VDVGAAVLFDCRVTGD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 SPPHFTHQPHDQIVALHSSGHVLLDCAASGWPQPDIQWFVNGRQLLQSTPS-LQLQANGS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPG-----RHTVSGGSLLMARAEKSDE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 XTYMCVATNSAGHRESRAARVSIQE----PQDYTEPVELLAV---RIQLENVTLLNPDPA 228
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                                                 VAVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALOP-GRHTV-SGGSLLMARAEKSDEXT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.2%; Score 253; DB 2; Length 15 Best Local Similarity 30.3%; Pred. No. 1.9e-11; Matches 80; Conservative 33; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                PKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR
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%;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
f. Exp. Med. 168, 1523-1530, 1988
i,Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region how presence number: JL0051; MUID:89035978; PMID:2972792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:120138; OMIM:179590
A;Map position: 1p34-1p34
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoprotein; phosphoric monoester hydrolase; transmembrane
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403-489/Domain: fibronectin type III repeat homology <FN3B>
550-583/Domain: fibronectin type III repeat homology <FN3D>
558-688/Domain: fibronectin type III repeat homology <FN3D>
588-798/Domain: fibronectin type III repeat homology <FN3D>
780-893/Domain: fibronectin type III repeat homology <FN3F>
780-893/Domain: fibronectin type III repeat homology <FN3F>
71001-1078/Domain: fibronectin type III repeat homology <FN3F>
71271-1274/Domain: fibronectin type III repeat homology <FN3F>
71271-1274/Domain: fibronectin type III repeat homology <FN3F>
71271-1274/Domain: fibronectin type III repeat homology <FN3H>
71271-1274/Domain: intracellular #status predicted <INM>
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;1-16/Domain: signal sequence #status predicted <SIG>
;17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
;17-1250/Domain: extracellular #status predicted <EXT>
;17-99/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
1165-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
11654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
1164-97,146-197,243-288/Disulfide bonds: #status predicted
1107,240,285,711,956/Binding site: carbohydrate (Asn) (covalent) #status predicted
11538/Active site: Cys (phosphocysteine intermediate) #status predicted
11644/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----MVPPDPHHLL
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,Residues: 1-1897 <STR>
;Cross-references: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.1.3.48)
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                                                                                                                                                                                                                                                                                                                                                                                                           : :|:||: | |||||||| | | : ::
193 QIESSEESDQGKYECVATNSAGTRYSAPANLYVR 226
                                                                                                                                                                                                                                                                                                                                                       LMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :139-199/Domain: immunoglobulin homology <IMM2>:236-290/Domain: immunoglobulin homology <IMM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Accession: S03841
;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S03841; JL0051
                       |::| :||
86 GAGSVLRIQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: GDB: PTPRF; LAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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C;Species: Ratus norvegicus (Norway rat)
C;Date: 20-Pb-1995
C;Accession: S46216; 821251; A1032, A31154
C;Date: 20-Pb-1995
R;Accession: S46216; 821252; A41032, A31154
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem, J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phc
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Residues: 1-1898 c.ZHA>
A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by thre
A;Residues: nucleic acid sequence not shown
A;Residues: 23226; MUID:92287069; PMID:1599438
A;Accession: S23226
A;Atlue: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 c.HAS>
A;Accession: S2322
A;Atlue: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 c.HAS>
A;Title: Cloning, bacterial expression, purification, and characterization of the cytopl
A;Accession: A4002
A;Accession: A4003

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Affocession: Affocession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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31.8%; Pred. No. 6.3e-10;
ive 37; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.83
Matches 68; Conservative
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A;Residues: 1-296,'T', 298-1040 <HA2>
A;Cross-references: EMBL:X68274
R;Tsiotra, P.C.; Karagogeos, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley, Genomics 18, 562-567, 1993
A;Title: Isolation of the cDNA and chromosomal localization of the gene (TAXI) encoding A;Reference number: A49356; MUID:94140354; PMID:8307567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology C;Keywords: cell adhesion; glycoprotein
F;1-28/Domain: signal sequence #status predicted <SIG>F;29-1040/Droduct: axonal glycoprotein TAG-1 #status predicted <MAT>F;25-1040/Domain: immunoglobulin homology <IFMUL>F;341-397/Domain: immunoglobulin homology <IFMUL>F;76,198,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (coval
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A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;MOlecule type: DNA
A;Residues: 1-5175 <WIL>
A;Residues: 1-5175 <WIL>
A;Residues: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 KAHEGWGVMLPCNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTTGNLXIARTNASDLG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 TYMCVATNSAGHRE-----SRAARVSIQ------EPQDYTEPVELLAVRIQLE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 29.5%; Pred. No. 1e-09; Similarity 29.5%; Pred. No. 1e-09; Noservative 38; Mismatches 99; Indels 5:
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R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 NVTLLNPDPAEGPKPRPAVWLXW-KVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFAFGNPVPR-----IKWRKVDG 278
                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1001,'G',1003-1040 <TSI>A;Cross-references: GB:X67734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: GDB:TAX; TAX1
A,Cross-references: GDB:138782
A,Map position: 1q32-1q32
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Best Local Simil
Matches 79; C
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Cipture: 20-Peb-1995 #sequence_revision 23-Mar-1995 #text_change 24-Sep-1999
Cipture: 20-Peb-1995 #sequence_revision 23-Mar-1992
Ridaeler, To the EMBL Data Library, September 1992
A;Reference number: 835508
A;Reference number: 835508
A;Residues: 10-104 cHAS.
A;Residues: 1-1040 cHAS.
A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                             GFPSIDMGPQLKVVEKARTATMLCA-AGGNPDPEISWFKDFLPVDPATSNGRIKQLRSGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 VIMSP-----TKTQDAGVYQCLASNPVGTVVSKEAVLRFGFLQE-FSKEERDPVK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 V-VGEQPTLECGPPWGHPEPTVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 THEGWGVMLPCNPPAHYPGLSYRWLLANEPPNFIPTDGRHFVSQTTGNLYIARTNASDLGN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    axonal glycoprotein TAG-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 21-Jan-2000
C;Accession: A34695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 230.5; DB 2; 28.8%; Pred. No. 6.5e-10; ive 41; Mismatches 98;
                                                                                                                                                                                                                LLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 199
                                                                                                                                                                                                                                                          transient axonal glycoprotein TAG-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 VTLLNPDPAEGPKPRPAVWLXW-KVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 FAFGNPVPR-----IKWRKVDG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternate names: axonin-1
.Species: Homo sapiens (man)
bate: 20-Feb-1995 #sequence_revis:
.Accession: S35508; S28830; Ā49356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 28.8% 18 77; Conservative
                                                   117 RDMVAVVGEQF-
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Best Local Si
Matches 77
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Mismatches 104;
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---VTWK-RGDDAVPNDSR 3436
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      35;
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         74; Conservative
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Clabte: 11-Jan-2000 #text_change 18-Feb-2000
RlyOgel, B.E.; Hedgecock E.M.
RlyOgel, B.E.; Hedgecock E.M.
RyOgel, B.E.; Handlated from GB/EMBL/DDBJ
A,Rogeldues: 1-5198 k.W.Good
RyOgel, B.E.; Handlated from GB/EMBL/DDBJ
RyOgel, B.Ype: DNR
RyOgel, B.Ype: DNR
RyOgel, B.Ype: DNR
RyOgel, B.E.; Handlated from GB/EMBL/DDBJ
RyOgel, B.Ype: DNR
RyOgel, B. M. RyOgel, B. M. RyOgel, B. M. Ryogel, B. Ryogel, Ryogel,
A;Gene: CESP:F15G9.4a
A;Map position: X
A:Introne 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2667/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4991/1; 5011/1; 5077/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VLHIRNATRADEGKYSCIASNEAGTAV---ADFLIDVFTKPTFETTFN 3310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                62 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVL-REDFQIQPRDMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VATNSAGHRE----SRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 235
                                                                                                                                                                                                                                                                                                               4 PPQILVHPQDQLFQGP--GPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3370 VATNSYGDSEQDFKVNVYTKPYIDETIDQT-PKAVAGGEIILKCPVLGNPTPT---
                                                                                                                                                                                                                                                                                                                                                  3216 PPRI--EDEERVLQGKEGNTYMVHCQVTGRPVPYVTWKRNGKEIEQFNP----
                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                        Length 5175;
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                                                                                                                                                                                  Query Match 15.5%; Score 228; DB 2; Length 51: Best Local Similarity 28.6%; Pred. No. 6e-09; Matches 74; Conservative 35; Mismatches 104; Indels
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Pred. No. 6.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AVWLXWKVSGPXRLPNLTR 254
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28.6%;
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Best Local Similarity
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Alternate names: periecan Species: Museulus (house mouse)
Species: Mus musculus (house mouse)
Spate: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Nov-1999
Accession: S18252; A31917; B31917; S66660
Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Hailol. Chem. 266, 22939-22947, 1991
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, Residues: 1-3707 < NUO>
, Cross-references: EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
, Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass:
, Biol. Chem. 253, 16379-16387, 1988
, Title: Identification of cDNA clones encoding different domains of the basement membra:
, Reference number: A92680; MUID:89034110; PMID:2972708
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"Residues: 1272-1274, X', 1276, X', 1278-1279 cSCH>
"Residues: 1272-1274, X', 1276, X', 1278-1279 cSCH
"Residues: 1272-1274, X', 1276, X', 1278-1279 cSCH
"Residues: 1272-1279, EGP homology cLDL1>
"1285-1279, Momain: LDL receptor ligand-binding repeat homology cLDL3>
"1285-1359/Domain: LDL receptor ligand-binding repeat homology cLDL3>
"1286-403/Domain: LDL receptor ligand-binding repeat homology cLDL3>
"1286-1174, Momain: LDL receptor ligand-
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5,3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;3464-3492/Domain: EGF homology <EGF7>
F;256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted
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**Residues: 940-1601 <NO2>
**Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
**Accession: B31917
**Residues: 1870-2600 <NO3>
**Residues: 1870-2600 <NO3>
**Residues: 1870-2600 <NO3>
**Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
**Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
**Title: Structural properties of recombinant domain III-3 of perlecan containing of recombines: $66460; MUID:95377282; PMID:7649154
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              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VATNSAGHRE----SRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC
4 PPQILVHPQDQLFQGP--GPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
                                                                                                                                          3216 PPRI--EDEERVLÓGKEGNTYMVHCQVTGRPVPYVTWKRNGKEIEQFNP
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                                                                                                                                 2433 PPTVSVLP-----EGPVHVKMGKDITLECISSGEPRSSPRWTRLGIPVKLEPRMFGLMNS 2487
                                                                                                                                                                                                                           2529 APGTPQVQVEESELTLEAGHTATLHCSAT-GNPPPTIHWSKLRAPL---PWQHRIEGNTL 2584
                                                                                                                                                                                                                                                                                          106 AVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSL 165
                                                                                                                                                                                                                                                                     166 LMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYT-----BPVELLAVRIQL 217
                                                                4 PPQILVHPQDQLFQGPGPARM----SCRASGQPPPTIRWLLNGQPLSMVP----PDP 52
                                      66; Gaps
Query Match 15.3%; Score 225; DB 2; Length 3707; Best Local Similarity 27.6%; Pred. No. 7.1e-09; Matches 72; Conservative 37; Mismatches 86; Indels 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3218 EAELTVEAGHTATLRCSAT-GSPAPTIHWSKLRSPL---PWQHRLEGDTLIIPRVAQQDS 3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LLQPPARGHAHDGQALSTDLGVYTCEASNRLGTA-----VSRGARLSVAVLREDFQIQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 175
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                                                                                                                                                                                                                                                                                                                              SEA.

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 4.

LG-LIKE C2-TYPE 1.

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 5.

LAMININ EGF-LIKE 6 (TOOMPLETE).

LAMININ EGF-LIKE 6 (TOOMPLETE).

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 7.
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| B GF-LIKE 4 (INCOMPLETE) |
| B GF-LIKE 5 (N-TERMINAL) |
| B GF-LIKE 5 (C-TERMINAL) |
| B GF-LIKE 5 (C-TERMINAL) |
| B GF-LIKE 6 |
| B GF-LIKE 7 |
| B GF-LIKE 7 |
| B GF-LIKE 9 |
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| B GF-LIKE 10 |
| B GF-LIKE 10 |
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| B GF-LIKE 13 |
| B GF-LIKE 14 |
| B GF-LIKE 15 |
| B GF-LIKE 16 |
| B GF-LIKE 17 |
| B GF-LIKE 17 |
| B GF-LIKE 18 |
| C-TYPE 3 |
| B C2-TYPE 4 |
                                                                                                                                                                                           Signal; Basement membrane; Proteoglycan; Repeat, Glycoprotein; Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain; Extracellular matrix; EGF-like domain; Disease mutation.

1 POTENTIAL.
                                                                                                                                                                                                                                                                                         BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN.
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C2-TYPE 8.

C2-TYPE 10.

C2-TYPE 11.

C2-TYPE 12.

C2-TYPE 14.

C2-TYPE 14.

C2-TYPE 14.

C2-TYPE 15.

C2-TYPE 16.
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C2-TYPE 6.
                PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 6.
PROSITE; PS500315; IG_IKE; 22.
PROSITE; PS500315; IAM G DOMAIN; 3.
PROSITE; PS01248; IAMININ TYPE_EGF; 11.
PROSITE; PS50024; IAMININ TYPE_EGF; 11.
PROSITE; PS50024; SEA; 1.
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SMART: SM00200; SEA: 1
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Db 3274 GQYICNATSPAGHAEATII-LHVESPPYATTVPEHASVQAGETVQLQCL-----AHGT 3325
Qy 232 KPRPAVMLXWKVSGPXR 248
Db 3326 PPLTFQWSRVGSSLPGR 3342
Search completed: January 30, 2004, 15:55:15
Job time: 10.5337 secs
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PRINTS; I
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SMART; S
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 SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
MEDLINE=20553141; PubMed=111018S0;
Micole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
Hentati F., Fontaine B.;
"Perlecan, the major proteoglycan of basement membranes, is altered in
patients with Schwarzz-Jampel syndrome (chondrodystrophic myotonia).";
                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.

TISSUB=COlon, and Skin;

MEDLINE=92235084; PubMed=1569102;

MEDLINE=92235084; Debmed=1569102;

Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;

"Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSPGZ/perlecan). A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";

J. Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                                     core protein: a elements of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
-!- FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.
-!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xi H.F., Iozzo R.V.;
"Heparan sulfate proteoglycan of human colon: partial molecular
"Cloning, cellular expression, and mapping of the gene (HSPG2) to the
short arm of human chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B., Tryggvason K.; "Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene (HSPG2) to 1p36.1-->p35 and identification of Genomics 11:389-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.; "Structural characterization of the complete human perlecan gene and
                                                                                                                                                                                                                 "Human basement membrane heparan sulfate proteoglycan core protein: 467-kD protein containing multiple domains resembling elements of th low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor."; J. Cell Biol. 116:559-571 (1992).
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
        P98160; 016287; 09H3V5; 01-0CT-1996 (Rel. 34, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 15-FBB-2003 (Rel. 41, Last annotation update) Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).
PRT; 4391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fibrosarcoma;
MEDLINE=92120660; PubMed=1685141;
                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=92112994; PubMed=1730768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91365376; PubMed=1679749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1016-1470 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 890-1396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 26:480-483 (2000).
                                                                                                                                                                                                      Kallunki P., Tryggvason K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 10:673-680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-21 FROM N.A.
STANDARD;
                                                                                                          Homo sapiens (Human)
                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its promoter.";
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                                                                                            HSPG2
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                                                                                                                                                                                         -I-DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder characterized by permanent myotonia (prolonged failure of muscle relaxation) and skeletal dysplassia, resulting in reduced stature, kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
-I-SIMILARITY: Contains 4 LDL-receptor class A domains.
-I-SIMILARITY: Contains 11 laminin EGF-like domains.
-I-SIMILARITY: Contains 21 laminin IV domains.
-I-SIMILARITY: Contains 3 laminin GP-like domains.
-I-SIMILARITY: Contains 3 laminin G-like domains.
-I-SIMILARITY: Contains 1 SEGF-like domains.
-I-SIMILARITY: Contains 1 SEGF-like domains.
-I-SIMILARITY: Contains 1 SEA domain.
                             membrane components such as laminin, prolargin and collagen type
dimers or stellate structures. It interacts with other basement
                                                                                -1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
-1- PTM: CONTAINS THREE HEPRARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteoglycan; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002172; LDL_receptor_A. IPR000082; SEA_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S76436; AAB21121.2; -.
EMBL; L22078; -; NOT ANNOTATED_CDS.
PIR; A38096; A38096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig_v.; Laminin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005206; F:heparin sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laminin_EG
Laminin_G.
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m; PF00053; laminin B; 3.
n; PF00054; laminin G; 3.
n; PF00057; ldl_recept_a; 4.; PF01390; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL445795; CAC18534.1; -. M64283; AAA52699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro, IPR000742; EGF 2.
Interpro, IPR001438; EGF II.
Interpro, IPR006209; EGF like.
Interpro, IPR006210; IEGF.
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PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X62515; CAA44373.1; -. EMBL; M85289; AAA52700.1; -.
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IG; 22.
IGc2; 21.
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IPR003598; IG.c2.
IPR003006; IG_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00740; 1EDM.
Siena-2DPAGE; P98160;
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SM00192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 142461;
MIM; 255800;
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PGBM_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-FROT entry is copyright. It is produced through a collaboration the Ewrent the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              Pearon B.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,
Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,
                                                                                                                                                                                                                                                                                                                                              VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.
MEDLINE=94243823; Pubmed=8187090;
Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;
"Point mutations and all-alic deletion of tumor suppressor gene DCC in human esophageal squamous cell carcinomas and their relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                 CANCER ES. 54:3007-3010(1994).

-!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
-!- SUBCELLULAR LOCATION: TYPE I membrane protein.
-!- SUBCELLULAR LOCATION: TYPE I membrane protein.
-!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM AND IN DIFFERENTATED CELL TYPES OF THE INTESTINE.
-!- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO DIFFERENTIANTE NIVO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC EXPRESSION, INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR POINT MUTATIONS NAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS METASTASIS OF OSSOPHAGRAL SQUAMOUS CELL CARCINOWAS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 4 immunoglobulin-like C2-type domains. SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                       GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.
MEDLINE-94245241; PubMed-8188295;
Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,
Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;
"The DCC gene: structural analysis and mutations in colorectal
                                                                                                            SEQUENCE OF 107-472 FROM N.A. (SCRAMBELD EXONS).
MEDLINE=91121517; PubMed=1991322;
Nigro J.M., Cho K.R., Fearon E.R., Kern S.E., Ruppert J.M.,
Oliner J.D., Kinzler K.W., Vogelstein B.;
Carambled exons.;
Cell 64:607-613(1991).
                                                        "Identification of a chromosome 18q gene that is altered in colorectal cancers.";
Science 247:49-56(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004888; F:transmembrane receptor activity; TAS. GO; GO:0007409; P:axonogenesis; TAS. GO; GO:000611; P:induction of apoptosis; TAS. GO; GO:0007048; P:onocogenesis; TAS. InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M32288; AAA52175.1; ALT_SEQ.
M32290; AAA5176.1; -.
M63709; AAA52177.1; -.
M63700; AAA5178.1; -.
M63702; AAA52179.1; -.
MEDLINE=90100559; PubMed=2294591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X76132, CAA53735.1; -. EMBL, M32292, AAA35751.1; -. EMBL, M32286; AAA52174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M63700; AAA52178.1; EMBL; M63702; AAA52179.1; EMBL; M63718; AAA52180.1; EMBL; M63698; AAA52181.1; -PIR; A54100; A54100.
                                                                                                                                                                                                                                                                                                    carcinomag.";
Genomics 19:525-531(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:2701; DCC.
                                                                                                                                                                                                                                                                                                                                                                                                                             metastasis."
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EMBL;
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206 DIGIYRCSARN---PASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVVAIEGKDAVLECC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 VS-GYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNVTDDDSGMYTCVVTYKNENISA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 RAARVSIQEPQDYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 DLGVYTCEASNRLGTAVSR-GARLSVAVLRED-----FQIQPRDMVAVVGEQFTLECG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 PPWGHPEPTVSWWKDGKPLALQPGRHTVSGGS-LLMARAEKSDEXTYMCVATNSAGHRES 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 SAELTVLVPPWFLNHPSNLYAYESMDIEFECTV-----SGKPVPTV--NWMKNGDVV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 MSCRASGOPPPTIRWLLNGOPLSMVPPDPH-HLLPDGTLLL--LOPPARGHAHDGQALST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M -> T (in oesophageal carcinoma).
Frid=VAR_003909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P -> H (im a colorectal carcinoma)
/FTtd=VAR 003911.
MISSING (IN REF. 3).
MISSING (IN REF. 3).
MISSING (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                   bulin domain; Transmembrane; Signal;
Disease mutation; Polymorphism.
                                                                                                                                                                                                       TUMOR SUPPRESSOR PROTEIN DCC. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Indels
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                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
PIBRONECTIN TYPE-III 5.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC...
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FTId=VAR_003910.
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                                                                                                                                                                                                                                                  POTENTIAL.
InterPro; IPR003598; Ig_c2.
InterPro; IPR00306; Ig_MHC.
Pfam; PP00041; fn3; 6.
Fram; PP00041; fn3; 6.
PRINTS; PR00004; FNTYPEIII.
SWART; SW00060; FN3; 6.
SWART; SW00060; FN3; 6.
SWART; SW00408; IGc2; 3.
PROSITE; PS50835; IG LIKE; 4.
Clycoprotein; Immunoglobulin don
Repeat; Anti-oncogene; Disease ISIGNAL
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329
421
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CONFLICT
CONFLICT
SEQUENCE
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AD DCC H
AD DCC H
DD O1-NO
DT 01-NO
DD 15-SB
DE TUMOR
GN DCC.
COC BUKAR
COC MAMMA
COC
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOId=P97798-5; Sequence=VSP 002597;
Note=Expression developmentally regulated;
TISSUE SPECIFICITY: Widely expressed.

TISSUE SPECIFICITY: Widely expressed.

DEVELOPMENTAL STAGE: EXPRESSED UBIQUITUGELY THROUGHOUT THE MID TO
LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION
IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE
E15.5 MOUSE NEURAL TUBE, AS WELL AS IN THE VENTRICULAR ZONE OF
THE MESENCEPHALON AND RHOMBENCEPHALON. ISOFORMS 3 AND 4 ARE
EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN E11.5
                                                                     and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0014; "ENTYPEIII.
SWART; SMO0060; FN3; 6.
SWART; SM00408; IGG2; 4.
PROSITE; PSS0835; IG LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
                MEDLINE=97407661; PubMed=9264410;

Keeling S.L., Gad J.M., Cooper H.M.;

"Mouse negogenin, a DCC-11ke molecule, has four splice variants and i "Mouse negogenin, a DCC-11ke molecule, has four splice variants and i concepend widely in the adult mouse and during embryogenesis.";

L. C. PUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADMESION C. IS UNCECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.

C. I. ALTERNATIVE PRODUCTS:

C. I. ALTERNATIVE PRODUCTS:

C. I. ALTERNATIVE PRODUCTS:

C. Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 4 immunoglobulin-like C2-type domains. SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND E16.5. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P97798-3; Sequence=VSP 002595;
Note=Expression developmentally regulated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P97798-4; Sequence=VSP 002596;
Note=Expression developmentally regulated;
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P97798-2; Sequence=VSP_002594;
                                                                                                                                                                                                                                                                                                                                     IsoId=P97798-1; Sequence=Displayed;
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SIGNAL 136 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003961; FN III.
InterPro; IPR003962; FNIII subd.
InterPro; IPR00310; Ig-like.
InterPro; IPR003598; Ig-c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00041; fn3; 6.
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MGD; MGI:1097159; Neol.
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11157
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63 LLQPPARGHAHDGQALSTDLGVYTCEAS-NRLGTAVSRGARLSVAVLREDFQIQPRDMVA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tumor suppressor protein DCC precursor (Colorectal cancer suppressor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDLINE-95011532; PubMed-7926722;
Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,
Vogelstein B.;
"The DCC gene product in cellular differentiation and colorectal
tumorigenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%; Score 209; DB 1; Length 1493; 29.5%; Pred. No. 1e-08; tive 32; Mismatches 99; Indels 2:
                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP 002595.

1086 1096 Missing (in isoform 4).
/FTId=VSP 002596.

1279 1331 Missing (in isoform 5).
/FTId=VSP 002597.

1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;
                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
Missing (in isoform 2).
FYIG-VSP 002594.
Missing (in isoform 3).
FYIG-VSP 002595.
                                                                                                                                                                             (GLCNAC. . . )
(GLCNAC. . . )
(GLCNAC. . . )
(GLCNAC. . . )
           FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 6
FIBRONECTIN TYPE-III 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 XTYMCVATNSAGHRESRAARVSI-QEPQDYTEPVELL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 GLYRCIVESGGPPKFSDEAELKVLQDPEEIVDLVPLM 264
                                                                                          POLY-VAL.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
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P43146;
01-NOV-1995 (Rel. 32, Created)
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SEQUENCE OF 1-750 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Conservative
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 64; Conser
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373
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                                                                                                                                     DOMAIN
                                                                                                                                                                                             DOMAIN
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NEO1_MOUSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration devenen the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in oway modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative initiation;

Comment=2 isoforms, A (shown here) and B, are produced by alternative initiation at met-1 and met-85;

TISSUE SPECIFITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE BEVELOPING BRAIN WITH EXPRESSED FOUND IN TESTIS, HEART AND THYMUS.

BEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.

ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.

DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS EXPRESSED DUBING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.

SUBFAMILY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P70211-1; Sequence=Displayed;
Note=Isoform B is produced by alternative initiation at Met-85
                                                                                                                                                                                             cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.; "Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo."; [2]
                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 4 immunoglobulin-like C2-type dt SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Brain;
Cooper H.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE. SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                     Last sequence update)
Last annotation update)
             1447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P70211-2; Sequence=VSP_002501;
                                                                                                                                                                             ົວ
                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upi
15-SEP-2003 (Rel. 42, Last annotation utils-SEP-2003 (Rel. 42, Last annotation utils of precursor.
                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS A; B AND
                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=96112625; PubMed=8570174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III subd.
InterPro; IPR007110; Ig-li\overline{k}e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR001598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00041; fn3; 6.
Pfam; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; 6.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X85788; CAA59786.1; -. HSSP; P56276; 1TLK.
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:94869; Dcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoform A;
           MOUSE
                                                                                                                                                                                                                                                                                          REVISIONS
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 PWGHPEPTVSWWKDGKPLALQPGRHTVSGGS-LLMARAEKSDEXTYMCVATNSAGHRESR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 S-GYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNVTDDDSGTYTCVVTYKNENISAS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AARVSIQEPQDYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AELTVLVPPWFLNHPSNLYAYESMDIEFE-----CAVSGKPVPTV--NWMKNGDVVI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLGVYTCEASNRLGTAVSRGARLSVAVLRED-----FQ1QPRDMVAVVGEQFTLECGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSCRASGOPPPTIRWLLNGQPLSMVPPDPH-HLLPDGTLLL--LQPPARGHAHDGQALST
                                 ISOFORM A. ISOFORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Gaps
   Alternative initiation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0D1F1097C22D5B9F CRC64;
                                 TUMOR SUPPRESSOR PROTEIN
                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                   FIRRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...)
                                                                                                                           IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 14.2%; Score 209; DB 1; Local Similarity 27.7%; Pred. No. 9.6e-09; Les 67; Conservative 37; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                      940
1117
212
310
Repeat; Anti-oncogene;
SIGNAL 1 25
CHAIN 26 1447
                               16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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PS 374
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                                                              INIT MET
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND REVISION TO 834.

Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;

Submitted (NOV-2001) to the EMBL/GenBank/DDB databases.

-!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY

THE CAPALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE
PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROGRESSION MARKER.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID
GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN
EXTHROLUCKHARA CELLS. BUT NOT EXPRESSED IN COLON.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
RECEPTOR SUBFAMILY.
SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                      SEQUENCE FROM N.A.

TISSUE=Colon carcinoma, and Placenta;

MEDLINE=96074849; PubMed=7478540;

MOSSIE K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A.;

"Colon carcinoma kinase-4 defines a new subclass of the receptor

tyrosine kinase family.";

Oncogene 11:2179-2184(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601890; -.

Or) GO:0005886; C:plasma membrane; TAS.

GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.

GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_MHC.

InterPro; IPR003019; Prot Kinase.

InterPro; IPR00119; Prot Kinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR00145; IPR Prot Finase.

InterPro; IPR00147; IPR001485; Tyr_pkinase.
           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              MEDLINE=97037064; PubMed=8882711; Park S.K., Lee H.-S., Lee S.-T., The Medical Fark Characterization of the human full-length PTK7 cDNA encoding a receptor protein tyrosine kinase-like molecule closely related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J42521; AAC50484.2; ---
EMBL; AF44716; AAL39062.1; ---
EMBL; AF447126; AAL39062.1; JOINED.
EMBL; AF447189; AAL39062.1; JOINED.
EMBL; AF447162; AAL39062.1; JOINED.
EMBL; AF447167; AAL39062.1; JOINED.
EMBL; AF447170; AAL39062.1; JOINED.
EMBL; AF447170; AAL39062.1; JOINED.
EMBL; AF447177; JAL39062.1; JOINED.
EMBL; AF447177; JAL39062.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                          Biochem. 119:235-239(1996).
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sapiens (Human)
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                         chick KLG.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:
MIM; 601890;
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117 RDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEX 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R--VFTAGSEERVTCLPPKGLPEPSV-WWEHAGVRLPTHGRVYQKGHELVLANIAESDAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 PDGTLLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQ-PLSMVPPDPH----HLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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PRINTS; PRO0109; TYRKINASE.
Prodom; PR00109; TYRKINASE.
Prodom; PR00109; TYRKINASE.
SMART; SM00408; IGc2; 5.
SMART; SM00219; TYKE.
SMART; SM00219; TYKE.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00239; RECEPTOR TYR KIN 11; FALSE NEG.
Receptor; Transmenbrane; Signal; Glycoprotein; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                        TYROSINE-PROTEIN KINASE-LIKE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

PROTEIN KIMASE; INACTIVE.

BY SIMILARITY.

BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1070 AA; 118260 MW; 47CDF25B8E3698A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYMCVATNSAGHRES----RAARVS--IQEPQD 203
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                                                                                                                                                                                                                                                                                           29.18;
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Matches 62; Conservative
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send an email to license@isb-sib.ch)
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                                                                                                                                   51 TPFYPLVEPVDTLSVRGSSVILNCSAYSEPSPKIBWKKDGTFLNLVSDDRRQLLPDGSLF 110
                                                                                                                                                                                                                                                                         ------FQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWW 145
                                                                                                                                                                                                                                                                                          225 SGGPPKYSDEVELKVLPDPEVISDLVFLKQPSPLVRVIGQDVVLPCVAS-GLPTPTIKMM 283
                                                                                                                                                                                                                                                                                                                             KDGKPLALQPGRHTTV--SGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQD 203
                                                                                                                                                                              :| :|
165 AGNGAILNCEVNADLVPFVRWEQNRQPLLLDDRVIKLPSGMLVISNATEGDGGLYRCVVE 224
                                                                                                                                                                                                                                                                                                                                                       284 KNEEALDTESSERLVLLAGGSLEISDVTEDDAGTYFCIADNGNETIEAQAELTVQAQPEF 343
                                                                                                          3 SPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLL
                                                                                                                                                              63 LLQPPARGHAHDGQALSTDLGVYTCEAS-NRLGTAVSRGARLSVA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92174898; PubMed=13116/5; Zuellig R.A., Rader M.B., Zuellig R.A., Rader C., Schroeder A., Kalousek M.B., Zuellig R.A., Rader C., Schroeder A., Kalousek M.B., And Halbach F., Osterwalder T., Inan C., Stoeckli E.T., Affolter H.-U., Fritz A., Hafen B., Sonderegger P.; The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immunoglobulin-like and fibronectin-type-III-like domains and glycosyl-phosphartidylinositol anchorage."; Bur. J. Biochem. 204:453-463(1992).-- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 4 fibronectin type III domains.
                                                    Query Match
14.5%; Score 214.5; DB 1; Length 1461;
Best Local Similarity 22.7%; Pred. No. 3.6e-09;
Matches 79; Conservative 39; Mismatches 117; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY
                                                                                                                                                                                                                                                                                                                                                                                  204 YTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPN 251
                                                                                                                                                                                                                                                                                                                                                                                                    344 LKQPTNIYA----HESMDIVFECEVTG-KPTPTV--KWVKNGDMVIPS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM OF NEURITIC MEMBRANE.
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Contactin 2 precursor (Axonin-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1036 AA
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MEDLINE=92174898; PubMed=1311675;
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                                                                                                                                                                                                                      NCBI_TaxID=9031;
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01-DEC-1992 (
15-SEP-2003 (
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            CONFLICT
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P28685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 SYQCVATNARGTVVSREASLRFGFLQE-FSAEERDPVKITEGWGVMFT--CSPPPHYPAL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE----- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 MSCRASGOPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Gaps
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Q13308; Q13417;
30-MAY-2000 (Rel. 39, Created)
15-SEP-2003 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : :::|: :::| | SKFSQLSLAAEDARQYAETROWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Indels
                                                                                                                                                                                                SMART; SM00060; FN3; 4.
SMART; SM00408; IGc2; 5.
PROSITE; PSS0835; IG_LIKE; 6.
Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
Cell adhesion; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; 08B80143BE779794 CRC64;
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PIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                                                                                                                                  REMOVED IN MATURE FOR 11 IG-LIKE C2-TYPE 1. IG-LIKE C2-TYPE 2. IG-LIKE C2-TYPE 4. IG-LIKE C2-TYPE 4. IG-LIKE C2-TYPE 5. IG-LIKE C2-TYPE 5. IG-LIKE C2-TYPE 6. IG-LIKE C2-TYPE 6. IG-LIKE C2-TYPE 6. IG-LIKE C2-TYPE 6. INGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                           OR 25 (POTENTIAL) ...
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14.5%; Score 213.5; DB 1
Best Local Similarity 30.7%; Pred. No. 2.9e-09;
Matches 70; Conservative 31; Mismatches 86
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                PIR; S22383; S22383.
PDB; ICS6; 19-MAY-00.
InterPro; IPR003961; NIII.
InterPro; IPR00710; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR03508; Ig_MHC.
Pfam; PF00041; fn3; 3.
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EMBL; X63101; CAA44815.1; -
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                                                                                                                                                                                                                                                            130 YKGNSAILNC-----EVNVDLAPFVRWEQDRQPLSLDDRVFKLPSGALLIGNATDTDG 182
                                                                                                                                                                                                                                                                                                      183 GFYRCVIESGGTPKYSEEAELKIL--POPEEPQSLVFVROPSSLTKVTGONAVFPCVAGG 240
                                                                                                                                                                                                               63 LLQPPARGHAHDGQALSTDLGVYTCEAS-NRLGTAVSRGARLSVAVLREDFQIQPRDMVA 121
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                                                                                                                                                                                                                                                                                     176 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVR--IQLENVTLIN---PDPAEG
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vielmetter J., Chen X.-N., Miskevich F., Lane R.P., Yamakawa K., Kozenberg J.R., Dreyer W.J.; "Molecular characterization human neogenin, a DCC-related protei and the mapping of its gene (NBO1) to chromosomal position 15q22.3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                             C. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 41:414-421(1997).
-!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Fetal brain;
MEDLINE=97236653; PubMed=9121761;
Meyerhardt JA., Look A.T., Bigner S.H., Fearon B.R.;
"Identification and characterization of neogenin, a DCC-related
                                                                                                                                        14.6%; Score 215.5; DB 1; Length 1443; 31.4%; Pred. No. 3e-09;
                                                                                                                                                          27; Mismatches 117; Indels
                                                                                                                       MW; 558C6795579C0E26 CRC64;
 FIBRONECTIN TYPE-III 6.
                                             (GLCNAC.
                                                                                 (GLCNAC.
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                                                               (GLCNAC
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
         SIMILARITY. SIMILARITY. SIMILARITY.
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TISSUE=Fetal brain;
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                                                                                                                                                                                                                                                                                                                         231 PKPRPAVWLXWKVSG 245
                                                                                                                                                                                                                                                                                                                                    241 ---FPTPYVRWTKNG 252
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                                                                                                                       158050
                                                                                                                                                Local Similarity 31.4%
hes 80; Conservative
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                           286
376
39
176
292
456
475
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NEO1 OR NGN.
Homo sapiens (Human).
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176
292
456
475
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700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                Isold=Q92859-2; Sequence=VSP_002593;
TISSUE SPECIFICITY: WIDELY EXPRESSED AND ALSO IN CANCER CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES SUBCELLULIAR LOCATION: TYPE I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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GO; GO:0005887; C:integral to plasma membrane; TAS.
InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III subd.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00041; fn3; 6.
Pfam; PF00047; ig; 4.
PRINTS; PR00041; FNYPEIII.
SMART; SM00408; IGC2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
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N-LINKED (GLCNAC. . .)
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
FOLY VAL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 2
                                                                                          Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                 IsoId=Q92859-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U61262; AAB17263.1; -. EMBL; U72391; AACS1287.1; -. HSSP; P02751; ITTF. Genew; HGNC:7754; NEO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY
                                                                                                                                                                                          Name=2;
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loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 DDRRQLLPDGSLFISNVVHSKHN-----KPDEGFYQCVATVDNLGTIVSRTAKLAVAGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 PDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEAS-NRLGTAVSRGARLSVAVL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 REDFOIOPRDMVAVVGEOFTLECGPPWGHPE----PTVSWWKDGKPLALQPGRHTVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 PR-FTSOPEPSSIYVGNSGILNC-----EVNADLVPFVRWEQNRQPLLLDDRIVKLPS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSI-QEPQDYTEPVELL--AVRIQLEN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|:::| : | | | | | : : | | : : | | : : | | : : | | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : : | : | : : | : | : : | : | : : | : | : | : : | : | : : | : | : : | : | : : | : | : | : : | : | : : | : | : : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SPPQ------ILVHPQDQLFQGPGPARMSCRASGQPPFIIRWLLNGQPLSMVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 221.5; DB 1; Length 1377;
; Pred. No. 9.4e-10;
37; Mismatches 109; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 1.
IG-RONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
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NEOGENIN.
EXTRACELLULAR (POTENTIAL)
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BY SIMILARITY.
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N-LINKED (GLCNAC...)
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modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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BY SIMILARITY
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                                                                                                                                    InterPro; 197, 171.
InterPro; 1PR003961; FN III.
InterPro; 1PR003962; FnIII subd.
InterPro; 1PR003598; 19_12.
InterPro; 1PR003598; 19_22.
InterPro; 1PR00306; 19_MHC.
Pfam; PP00041; fn3; 6.
PRINTS; PR00041; fn3; 6.
SWART; SM00660; FN3; 6.
SWART; SM00660; FN3; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 29.1%;
                                                                                                EMBL; U68726; AAB41100.1; -
HSSP; P56276; ITLK.
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NON TER
SIGNAL CHAIN
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                                                                                                                                                                                                                                                                                                                                              WEDLINE=95105243; PubMed=7806578;
Wielmetter J., Roman J.M., Dreyer W.J.;
Vielmetter J., Roman J.M., Dreyer W.J.;
Wielmetter J., Roman cell surface protein expressed during terminal armore and the processor molecule deleted in colorectal cancer.";
J. Cell Biol. 127:2092-2020(1994).
J. Cell Biol. 127:
                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEL, 107644; AAC59662.1; -.

R PIR, 150600; 150600.

R HASP, PIL1276; 2MFN.

R INTERPRO; 1FR003962; FN III.

R INTERPRO; 1FR003962; FN III.

R INTERPRO; 1FR003962; FN III.

R INTERPRO; 1FR003006; IG_C2.

R INTERPRO; 1FR003006; IG_MAC.

R PÉRN; PR00041; FN IYPEIII.

R SWART; SW00060; FN3; 6.

R SWART; SW004008; IG_C2.

R SWART; SW004008; IG_C2.

R PROSITE; PSS0835; IG_LIKE; 4.

R CG11 adhesion; Repeat; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUE=Embryonic brain;
                                                                                                (Rel. 40, Last sequence update) (Rel. 42, Last annotation update)
                                                                       (Rel. 40, Created)
                        · STANDARD;
                                                                                                                                             Neogenin (Fragment)
                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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307
422
522
616
720
835
CHICK
NEO1 CHICK
Q90610;
                                                                       16-OCT-2001
                                                                                              16-OCT-2001
15-SEP-2003
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TISSUE=Brain;
MEDLINE=97015074; PubMed=8861902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neogenin precursor (Fragment)
                                                                                                                                       15.1%;
                                                                                                                  229027
                                                                                                                                                  27.5%;
                                                                                                                                                          67; Conservative
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  253
298
553
616
666
666
721
774
915
962
1183
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                                                                                                                   Ä.
                                                                                                                                              Similarity
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  253
298
553
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1183
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16-OCT-2001
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P97603;
           CARBOHYD
CARBOHYD
CARBOHYD
                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                               112
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                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                      Query Match
Best Local
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                                                                                    CARBOHYD
   CARBOHYD
                                                                                               CARBOHYD
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 9 fibronectin type III domains.
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III 9.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                   FlyBase; FBgn0000464; Lar.
GO; GO:0008045; P:motor axon guidance; IMP.
GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00381; IYE PHOSPHATASE 1; 2.
PROSITE; PS0056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR PHOSPHATASE 2; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Cell adhesion; Immunoglobulin domain; Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 1.
FIRRONECTIN TYPE-III 2.
FIRRONECTIN TYPE-III 4.
FIRRONECTIN TYPE-III 4.
FIRRONECTIN TYPE-III 6.
FIRRONECTIN TYPE-III 6.
FIRRONECTIN TYPE-III 6.
FIRRONECTIN TYPE-III 6.
FIRRONECTIN TYPE-III 7.
FIRRONECTIN TYPE-III 7.
FIRRONECTIN TYPE-III 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                  InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR003963; FnIII subd.
InterPro; IPR003598; Ig -11se.
InterPro; IPR003598; Ig -12se.
InterPro; IPR00387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR00041; FN PP.
Fram; PP001041; fn3; 9.
Pram; PP00102; Y_phosphatase; 2.
PRINTS; PR00104; FNYYPEIII.
PRINTS; PR00104; FNYYPEIII.
SMART; SM00060; FN; 9.
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AAC47002.1; JOINED.
AAC47002.1; JOINED.
                                                                                                                             EMBL; M27700; AAA28668.1; -.
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SMART; SM00194; PTPc; 2.
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2029
128
224
316
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                                                                                                                                                                                                                                           P28827; 1RPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1403
                                                                                                                                                                   EMBL, U36851, P
EMBL, U36852, P
EMBL, U36853, P
EMBL, U36854, P
EMBL, U36855, P
EMBL, U36855, P
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U36850;
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DOMAIN
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DISULPID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ----PGTRVIEVGHTVLMTC-KAIGNPTPNIYWIKNQTKVDMSNPRYSLKDGFLQIENSR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSDEXTYMCVATNSAGHRESRAARVSI---QEPQDYTEPVE----LLAVRIQLENVTLL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 EEDQCKYECVAENSMGTEHSKATNLYVKVRRVPPTFSRPPETISEVMLGSNLNLSCIAVG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLL--PDGTL
                                                                                                                                                                                                                                                                                                                                              ; Score 222; DB 1; Length 2029;
; Pred. No. 1.3e-09;
39; Mismatches 104; Indels .34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.-Y.,
Culotti J.G., Tessier-Lavigne M.;
"Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
                                                                                                  (POTENTIAL)
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                           (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
(POTENTIAL)
                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                               MW; 536A0C794D3DC800
                                                                                                     (GLCNAC.
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(GLCNAC.
                        (GLCNAC.
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42, Last annotation update)
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N-LINKED
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                                                                 SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
IsoId=P23468-1; Sequence=Displayed;
Name=2, Synonyms=Kidney;
IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
Name=3; Synonyms=Fetal brain;
IsoId=P23468-3; Sequence=VSP_005150;
PTW: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
FROM THE TRANSMEMBRANE SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE DELTA.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BY SIMILARITY.

CLEAVAGE (POTENTIAL).

N-LINKED (GLCNAC. ..) (F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                    EMBL; L38929; AAC41749.1; -.
                                                                                                                                                                                                                  HSSP; P18052; 1YFO.
Genew; HGNC:9668; PTPRD.
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1290
1912
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1137
1618
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1553
11553
1178
254
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TRANSMEM
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CARBOHYD
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 QPRDMVAV-VGEQF-----TLECGPPWGHPEPTVSWWKDGKPL--ALQPGR---- 157
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--- (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.
--- (ATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
--- SUBSELLULAR LOCATION: Type I membrane protein.
--- SUBSELLULAR LOCATION: Type I membrane protein.
--- SUBSELICITY: SEECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                   2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLS-----MVPPDPHHLL
                                                                                                                                                                                                                                                                                                                                                                                                                           21 ETPPRFTRTPVDQTGVSGGVASFICQATGDPRPKIVWNKKGKKVSNQRFEVIEFDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 GSGSVLRIQP-----LRTPRDEAIYECVASNNVG-EISVSTRLT--VLRED-QI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90046860; PubMed-2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
"A family of receptor-linked protein tyrosine phosphatases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Canton-S;
MEDLINE=96178473; Pubmed=8598047;
Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase) (dLAR).
                                                                                                                                                                                609 1137 Missing (In isoform 3).
/FIGHEVSP 055150.
1178 1179 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
1912 AA; 214759 MW; 3AEBGED32182E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The transmembrane tyrosine phosphatase DLAR controls motor axon guidance in Drosophila.";
Cell 84:611-622(1996).
                                                                                                                                                                                                                                                                                                                                                     20;
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 -HTVSG----GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 222; DB 1; Length 1912; 32.5%; Pred. No. 1.3e-09; ive 37; Mismatches 67; Indels 56
                                                                                    Missing (in isoform 2).
/FTId=VSP 005148.
Missing (in isoform 2).
/FTId=VSP 005149.
                          (GLCNAC. . .)
(in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989)
                                                                   /FTId=VSP 005147
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                          N-LINKED
Missing (
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Matches 74; Conservative
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                                                                                           229
                                                                                                                                       783
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                          CARBOHYD
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                           VARSPLIC
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  CARBOHYD
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P16621;
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                                                                                                                                                                                                                                                                                                                                                               2433 PPTVSVLP-----EGPVHVKMGKDITLECISSGEPRSSPRWTRLGIPVKLEPRMFGLMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PPQILVHPQDQLFQGPGPARM----SCRASGQPPPTIRWLLNGQPLSMVP----PDP
                                                                                                                                                                                                                                                                                                                                                                                                                             HHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTA-----VSRGARLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 LMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYT------EPVELLAVRIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphatases.";

EMBO J. 9:3241-3252(1990).

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95204468; PubMed=7896816; MEDLINE=95204468; PubMed=7896816; Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.; Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=91006018; PubMed=2170109;
Krueger N.X., Streuli M., Saito H.;
"Structural diversity and evolution of human receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LAMININ EGF-LIKE 9 (N-TERMINAL).
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LAMININ EGF-LIKE 10.
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LG-LIKE C2-TYPE 2.
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R APPLICATION NUMBER: 60/084640
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R APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/084637
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FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
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APPLICATION UNDHER: 60/083322
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083559
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PLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/085579
APPLICATION NUMBER: 60/081838
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	È	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySe	rLeuProLeuLeuLeuLeuleulleMet 23
	qq	-	GGAGGAGACAGCCTCCTGGGGGGGCAGGGGTTC	CTCTGCTGCTCCTGCTCATCA
	È	24	4 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPh	4.
	අු	61		TAGTCCACCCCAGGACCAGCTGTTC 12
	ò	4	GlnGlyProGlyProAlaArgMetSe	0-
	셤	121	CAGGGCCCTGGCCTGCCAGGATGAG	CCTCAGGCCAGCCACCTCCCACCATC 18
	à	64	4 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu	(alproproAspProHisHisLeuLeu 83
	qq	181	-8	TGCCCCCAGACCCACACCACCTCCTG 24
	ò	84	4 ProAspGlyThr	LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 10
	qq	241	CCTGATGGGACC	CCCGGGGACATGCCCACGATGGCCAG 30
	Ş.	104	94 AlaLeuSerThrAspLeuGlyValTyrThrCysGlualaSerAsnArgLeuGlyThrAla	lualaSerAsnArgLeuGlyThrAla 12
	Ор	301	-0	AGGCCAGCAACCGGCTTGGCACGGCA 36
	ò	124	4 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAapPheGlnIleGlnPro	euArgGluAspPheGlnIleGlnPro 14
	qq	361		rcceceaearrrccaearccaecer 42
	٥'n	144		hrLeuGluCysGlyProProTrpGly 16
	qq	421	-	crcreaargreecceccreece 48
,	λ	164	4 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly	
	ą a	481		iddaaakcccreeccreeades
	ò	184	14 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***	laArgAlaGluLysSerAspGlu*** 20
	욥.	541	•	caagagcagagagagtgacgaagg 60
	ò	204	04 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal	isArgGluSerArgAlaAlaArgVal 22
	qq	601	-Æ	ATAGGGAGAGCCGCGCAGCCCGGGTT 66
	č	224	4 SerlleGlnGluProGlnAspTyrThrGlul	ProvalGlubeubeuAlaValArgileGln 24
	qa	661	1 rccarccadadccccadaacracacdada	ğ
	ζ	244	4 LeuGluAsnValThrLeuLeuAsnProAspProA	aGluGlyProLysE
	qq	721	cresaaarsteacacresreaacccesarccre	cagagggccccaag
	&	264	4 ValTrpLeu***TrpLysValSerGlyPro***-	ArgLeuProAsnLeuThrArgProCy 28

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PRIOR PILING DATE: 1998-04-08
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FILING DATE: 1998-03-31
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-31
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PLICATION NUMBER: 60/080334
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781 GTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCCCTGCCCAATCTTACACGGCCTTG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Tumas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wold, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
LIE REFERENCE: P2630P1C9
                                     283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
                                                                           841 Trcaegacccagacreccceegaecccaegaecrecereeccaege 889
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; Sequence 210, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Gurney, Austin L.
Hillan, Kenneth J
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Desnoyers, Luc
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                                                                                                                                                                                                                                Baker Kevin P
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PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR PELING DATE: 1998-04-30
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1
FILING DATE: 1998-04-28
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Length:
Matches:
Conservative:
Mismatches: Gaps: 2.9e-136 1550.00 98.65 98.32 96.39 Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.:

US-10-047-021-86 (1-303) x US-09-978-192A-210 (1-3716)

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	È	24	GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
	QQ	61	GGAGGCATGGCTCAGGACTCCCGGCCCCAGGTCCTAGTCCACCCCCAGGACCAGCTGTTC 120
	8 8	4 6	6
	g è	121	CAGGGCCCTIGGCCAGGGAIGAGCIGCCAAGGCTCAGGCCAGGC
,	; <u>d</u>	181	
	රු අු	84	ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
	& <u>.</u> €	104	AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla
	` & සි	124	14
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	<u>ک</u> و	164	HisproGluproThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnproGly 183
	60 qa	184 541	ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
	දු පු	204	ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
	රු දු	224	24
	oy Op	244	LeuGluasnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
	ço qa	264	Valirpleu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy 283
	& 8	283	BSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
	RESULT 7 US-09-999- Sequence Publication GENERAL APPLICP	-832/ Sion INFC NNT: NNT: NNT: NNT: NNT:	NESULT 7 1S-09-999-832A-210 1S Sequence 210, Application US/0999832A 1S Sequence 210, Application US/0999832A 1S Sequence 210, Application US/0999832A 1S SEQUENCE OF SEQ

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FILING DATE: 1998-04-29
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE SEPERENCE: PESSOPPIGS: CURRENT APPLICATION NUMBER: US/09/99,832A CURRENT FILING DATE: 2001-10-24 PRIOR APPLICATION NUMBER: (09/91885 PRIOR APPLICATION NUMBER: (00/6250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: (00/66249 PRIOR FILING DATE: 1997-11-03 PRIOR PILING DATE: 1997-11-03 PRIOR PILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: (00/66364 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: (00/06531 PRIOR PILING DATE: 1998-03-10 PRIOR PILING DATE: 1998-03-11 PRIOR APPLICATION NUMBER: (00/077641 PRIOR PILING DATE: 1998-03-11 PRIOR APPLICATION NUMBER: (00/07764) PRIOR PILING DATE: 1998-03-11 PRIOR PILING
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/079786
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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R APPLICATION NUMBER: 60/080333 R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081955
R APPLICATION NUMBER: 60/081817
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R APPLICATION NUMBER: 60/081049
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08 R FILING DATE: 1998-04-21

R APPLICATION UNMERS: 60/082704

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082804

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082700

R FILING DATE: 1998-04-22 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 PLICATION NUMBER: 60/080107 LING DATE: 1998-03-31 APPLICATION NUMBER: 60/081071 FILING DATE: 1938-04-08 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08 FILING DATE: 1998-04-08
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FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/083558 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569

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ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
                                                        CACCCAGAGCCCACACATCCATGGTGGAAAGATGGGAAACCCCTGGGCCCTCCAGCCCGGA
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                                                                                                                                                                                                                  ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly
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                         AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gertitsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Publication No. US20030004102A1
GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan
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US-09-978-189-210
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Mismatches:
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Matches:
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                    R FILING DATE: 1998-04-30

R APPLICATION NUMBER: 60/084366

R FILING DATE: 1998-05-05

R FILING DATE: 1998-05-06

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R APPLICATION NUMBER: 60/084441

R RILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084637

R APPLICATION NUMBER: 60/084639

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084640

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R APPLICATION NUMBER: 60/084643

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R APPLICATION NUMBER: 60/084633

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APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/085704
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APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-07
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PLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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PPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084627
                APPLICATION NUMBER: 60/081071
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| TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuclaic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuclaic TITLE REPREMENT: 2010-10-15.
| PRICE RILLING DATE: 2010-10-15.
| PRICE PARTICATION NUMBER: 09/91865 |
| PRICE PARTICATION NUMBER: 09/91865 |
| PRICE PARTICATION NUMBER: 00/06249 |
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APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
ENTER PROPERTION TEMOVED - See File Wrapper or Palm
SEQ ID NO 210
LENGTH: 3716
                                                                                                                                     SerileGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln
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PUBLICATION NO. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Beterin, David
APPLICANT: Bater in David
APPLICANT: Farrara, Nagoleon
APPLICANT: Ferrara, Nagoleon
APPLICANT: Fong, Sherman
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, Audrey
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
Napier, Mary A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; ORGANISM: Homo sapiens US-09-978-608A-210
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085582
PRIOR PELING DATE: 1998-05-15
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PRIOR PELING DATE: 1998-05-15
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PRIOR PILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                       APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630PICL5
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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SEO ID NO 210
                                                                                                                     Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                Napier, Mary A.
Pan, James,
Paoni, Nicholas F.
Roy, Margaret Ann
Shelron, David L.
Stewart, Timothy A.
Tumas, Daniel
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           Ferrara, Napoleon
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US-09-978-585A-210
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APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botstein, David APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc
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APPLICANT: Pan, James;
APPLICANT: Pani, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams P. Mickey
APPLICANT: Williams P. Mickey
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly
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                                                                                                                     HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly
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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Desnoyers, Luc
Eaton, Dan
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/079923
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PPLICATION NUMBER: 60/081071
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661 TCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAG 720
                                 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
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CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
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PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/06449
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-21
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; Sequence 210, Application US/09978403A
; Publication No. US20030050240A1
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ilvaroff, Ellen
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tewart, Timothy
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Hillan, Kenneth
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ao, Wei-Qiang
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Grimaldi, J. C
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480 180 240 103 300 360 143 420 163 900 99 243 720 263 780 840 120 123 203 223 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183 63 23 9 43 83 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln AlakeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCA ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro GTCAGCAGAGGCGCTCCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCT ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProFrpGly ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** SerileGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArglleGln GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 241 cereareseaccerrerecrecracascecerecesesearaseceaceareseceas CGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGC CACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAAACCCCTGGCCCTCCAGCCCGGA ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGAGCCGCGCAGCCCGGGTT recarceaggagecedaggaeracaeggagecreresgagerresgerereggaarreag LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 721 crecanantereacacrecreaaccecearcerecagaececeaagecraagecraagecraagecraagecraagecraagecraagecraagecraagec ValTrpLeu***TrpLygValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy Greridecticacticadadescendeceraceceracecerateracacecerac GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLleuIleMet 299 883 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg TTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG 292 US-10-047-021-86 (1-303) x US-09-978-403A-210 (1-3716) Matches: Conservative: Mismatches: Indels: Gaps: US-09-978-564A-210
i. Sequence 210, Application US/09978564A
i. Publication No. US20030050241A1
i. GENERAL INFORMATION: 1550.00 98.65% 98.32% 96.39% Percent Similarity:
Best Local Similarity:
Query Match:
DB: 541 24 121 181 84 104 301 124 361 144 421 164 481 184 204 601 224 661 244 264 781 283 841 RESULT 13 용 8 셤 ò à 8 à 유 8 ð 셤 셤 8 셤 ò 셤 ð 원 ે 셤 ð 셤 à 셤 a ò 8 8 à

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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-09
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, J. Christe., Austin L.
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** James P.
** Millam I.P.
** William P. P. Wood, William I.P.
** WOOD WILLIAM I.P.
** PELLONION NUMBER: 00/05250
** PELLON DATE: 1309-1113
** RING PAPLICATION NUMBER: 00/07450
** PRIOR PAPLICATION NUMBER: 00/07450
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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Gerber, Hanspeter
Ashkenazi, Avi
Baker, Kevin P.
Botstein, David
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Eaton, Dan
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                                                                                                          CCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAG
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ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Kuo, Sophia S.
Napier, Mary A.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       R APPLICATION NUMBER: 60/083742

R APPLICATION NUMBER: 60/083742

R FILING DATE: 1998-04-30

R FILING DATE: 1998-05-05

R FILING DATE: 1998-05-05

R FILING DATE: 1998-05-06

R FILING DATE: 1998-05-06

R R FILING DATE: 1998-05-06

R R FILING DATE: 1998-05-07

R PILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084639

R APPLICATION NUMBER: 60/084639

R APPLICATION NUMBER: 60/084640

R APPLICATION NUMBER: 60/084640
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R FILING DATE: 1998-05-07
R PILING DATE: 1998-05-07
R PILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
R PILING DATE: 1998-05-13
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
                 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 PILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500
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FILING DATE: 1938-05-07
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085573
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NTION NUMBER: 60/085697
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Best Local Similarity:
Query Match:
DB:
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PRIOR PELICATION NUMBER: 60/081049
PRIOR PLINIO DATE: 1998-04-08
PRIOR PLINIO DATE: 1998-04-09
PRIOR PLINIO DATE: 1998-04-09
PRIOR PLINIO DATE: 1998-04-09
PRIOR PLINIO DATE: 1998-04-09
PRIOR PLINIO DATE: 1998-04-15
PRIOR PLINIO DATE: 1998-04-12
PRIOR PLINIO DATE: 1998-04-22
PRIOR PLINIO DATE: 1998-04-29
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                                FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/084639
APPLICATION NUMBER: 60/080333
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CURRENT APPLICATION NUMBER: US/09/99,833A
CURRENT FILING DATE: 2001-0-24
PRIOR APPLICATION NUMBER: 00/66226
PRIOR APPLICATION NUMBER: 60/66226
PRIOR APPLICATION NUMBER: 60/6634
PRIOR APPLICATION NUMBER: 60/6634
PRIOR APPLICATION NUMBER: 60/6634
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PRIOR APPLICATION NUMBER: 60/0634
PRIOR APPLICATION NUMBER: 60/07450
PRIOR APPLICATION NUMBER: 60/07764
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07991
PRIOR PILING DATE: 1998-03-20
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FILING DATE: 1998-04-01
                                                                                                                                                   Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                     Shelton, David L.
Stewart, Timothy A.
                          Paoni, Nicholas F
Roy, Margaret Ann
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APPLICANT:
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781 GTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCTGCCCCAATCTTACACGCCCTTG 840
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121 CGGGACATGGTGGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGC 480
                                                                                                                                           184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***
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CURRENT APPLICATION NUMBER: US/09/981,915A

CURRENT PILING DATE: 2001-10-16

PRIOR PILING DATE: 2001-07-30

PRIOR PLING DATE: 1997-110-17

PRIOR PLING DATE: 1997-110-17

PRIOR PLING DATE: 1997-110-17

PRIOR FILING DATE: 1997-11-03
                                           164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly
                                                                                                                                                                                                                                                                                          601 ACCTACATGTGTGTGTGGCCACCAACAGGCGCAGGACATAGGGAGAGAGCGCGCAGCCGGGGTT
                                                                                                                                                                                                                                                                                                                                          SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValTrpLeu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy
                                                                                           CACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA
                                                                                                                                                                                                                                            ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal
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Publication No. US20030054986A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestow, David
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Kuo, Sophia S.
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGGTCTTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCAGCAGAGGCGCTCGGCTGTCGTCGTCCTCCGGGAGGATTTCCAGATCCAGCCT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGGAGACAGCCTCCTGGGGGGCAGGGTTCCCTGCCTCCTGCTCCTGCTCATCATG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIle 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 83
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
               R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084508

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084627

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

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PRIOR FILING DATE: 1998-04-15
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PRIOR PILING DATE: 1998-04-22
PRIOR PELLATION NUMBER: 60/082704
PRIOR PILING DATE: 1998-04-22
PRIOR PELLING DATE: 1998-04-22
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181 CGCTGGTTGCTGAATGGGCACCCCTGAGCATGGTGCCCCCAGACCCACACCTCCTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACAGCTTGGCACGGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGACATGGTGGTGGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 ACCTACATGTGTGTGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGGCAGCCCGGGTT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerileGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCCAGGACCAGCTGTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProAspGlyThrLeuLeuLeuLeuClnProProAlaArgGlyHisAlaHisAspGlyGln 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAGGAGACAGCCTCCTGGGGGGGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60
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Mismatches:
Indels:
Gaps:
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          PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PRILING DATE: 1998-05-15
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Search completed: January 31, 2004, 17:18:16 Job time : 345.352 secs

23

63

83

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein January 30, 2004, 15:52:09 ; Search time 14.6529 Seconds (without alignments) 1988.631 Million cell updates/sec Run on:

US-10-047-021-86 1608 Title: Perfect score:

1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB (Maximum DB (

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	transmembrane rece	dutt1 protein - mo			hypothetical prote	leukocyte antigen-	peroxidasin - frui	neurofascin - chic	tumor suppressor -	leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	axonal glycoprotei	transient axonal g	heparan sulfate pr	protein-tyrosine-p	plasmacytoma-assoc	protein-tyrosine-p	hypothetical prote	hemicentin precurs	BIG-1 protein - ra	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine k	neuroglian - fruit	neogenin - chicken
SUMMARIES	OI	T14160	T30805	T14316	T42405	T29549	S46216	S46224	S26180	151669	TDHULK	158148	S46217	S50893	A34695	A49356	S18252	A56178	A53449	C54689	T20992	T43290	158164	B48758	A48758	TDFFLK	150212	JC4593	A32579	IS0600
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عبق	ery	27.9	27.7	25.8	22.4	22.2	15.8	15.7	•	15.2	15.2	14.8		4	14.7	14.4	•	14.3	14.2	14.2	14.2	٠	14.1		14.1	13.8	13.7	13.5	13.4	13.4
	Score	448.5	445.5	414.5	360	356.5	ഗ	253	251	245	244.5	237.5	237.5	237.5	236.5	232	231.5	230	228	228	228	228	227.5	227.5	227.5	222	220.5	217.5	216	215.5
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1036	267	1447	4391	1328	946	1277	1880	6642	7962	1259	1268	1375	1091	1091	1260	
13.3	13.0	12.8	12.8	12.7	12.5	12.5	12.2	12.2	12.1	12.1	12.1	12.1	12.0	11.9	11.9	
214	209	206	206	205	201.5	201	195.5	195.5	195	194.5	194.5	194.5	193	191.5	191	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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transmembrane receptor protein Robol - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14160
R;Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.;
Cell 92, 205-215, 1998
A;Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam A;Reference number: 217897; MUID:98117249; PMID:9458045
A;Accession: T14160
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Molecule type: mRNÅ
A,Residues: 1-1651 <KLD>
A,Rosidues: 1-1651 <KLD>
A,Cross-references: BMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1
A,Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1
A,Description: Appears to function as the gatekeeper controlling midline crossing C;Keywords: transmembrane protein

Gape 6 Length 1651; Indels Query Match 27.9%; Score 448.5; DB 2; Best Local Similarity 42.2%; Pred. No. 2.8e-25; Matches 92; Conservative 31; Mismatches 86;

64 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP 123 84 28 QDSPPQILVHPQDQLFQCPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP ò 셤

DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144 85 ઠે 쉽

DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204 145 ઠે g

238 YVCVGTINNVGERESKVADVTVLERPSFVKRPSNLAVTV 275 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242 205 ઠ g

RESULT 2

dutil protein - mouse
N;Alternate names: transmembrane receptor protein Robol homolog
C;Species: Mus musculus (house mouse)
C;Accession: T30805
R;Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P.
R;Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P.
A;Description: The mouse homologue of human DUT1/H-robol gene: protein sequence and chr
A;Reference number: 220879
A;Accession: T30805

12;

Gaps

48;

Length 1273; Indels 9

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Rizallen, J.A.; Yi, B.A.; Bargmann, C.I.
2611 92, 217-227, 1998
A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp
A;Reference number: Z22160; MUID:98117250; PMID:9458046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HGEVKSNEGSLKLAMLREDFRVRPRTVQALGGEMAVLECSPPRGFPEDVVSWRKDDKELR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 IRWLLNGQPL--SMVPPDDPHHLLPD-GTLLLLQPPARGHAHDGQALSTDLGVYTCEASNR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 LGTAVSRGARLSVAVLREDPQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQP-GRHTV-SGGSLLIMARAEKSDEXTYMCVATNSAGHRESRAARVSI-----QEPQD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 YTEPVELLAVRIQLENVTLIANPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 MT------VDVGAAVLFDCRVTGDPQPQ----ITWK-----RKNEPMPVTRAYIAK 276
                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: AF041053; NID: 92804779; PIDN: AAC38848.1; PID: 92804780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-423 <NHA>
A;Redidues: 1-423 <NHA>
A;Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3
A;Experimental source: strain Bristol N2; clone ZK377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jr. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                      03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGSLPLLLLINGGM----AQDSPPQILVHPQDQLFQGPARMSCRASGQPPPT--
                                                                                                                                                                                                                                                                                                                                                                                 A, Description: sax-3 function is required at the time of axon guidance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: T29549
R, Mhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A, Description: The sequence of C. elegans cosmid ZK377.
A, Reference number: Z20639
                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%; Score 360; DB 2; L
32.7%; Pred. No. 7.7e-19;
tive 50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ZK377.3 - Caenorhabditis elegans
                                                                                                                                                                                      A;Accession: T42405
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 32.7'
Matches 101; Conservative
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DNRGLRIER 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 EARELRGQR 299
                                                                                                                                                                                                                                                          A; Residues: 1-1273 <ZAL>
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Matches 97; Conserv
                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: ZX377.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: T29549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                      A; Note: Bax-3
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                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                             C, Function:
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Datcesion: T14316
R;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, B.Y.H.P.
R;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, B.Y.H.P.
A;Reference number: Z17975
A;Accession: T14316
A;Accession: T14316
A;Accession: T14314
A;Molecule type: mRNA
A;Residues: 1-1344 <YUA>
A;Residues: 1-1344 <YUA>
A;Cross-references: EMBL:AF060570; NID:g4206385; PID:g4206386; PIDN:AAD11628.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQLQPR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                  28 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH-'--LLP 84
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1612 <WUM>
A;Residues: 1-1612 <WUM>
A;Cross-references: EMBL:X17793; NID:e1329712; PID:e1329713; PIDN:CAA76850.1
A;Experimental source: brain
C;Genetics:
A;Gene: duttl
A;Map position: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODSPPQILVHPODOLFQGPGPARMSCRASGOPPPTIRWLLNGQPLSMVPPDP--HH-LLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YMCVATNSAGHRESRAAR-VSIQEPODYTEPVELLAVRIQLENVTLLNPDPAE-----
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                      DB 2; Length 1612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.8%; Score 414.5; DB 2; Length Best Local Similarity 39.9%; Pred. No. 7.4e-23; Matches 101; Conservative 27; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
                                                                                                                                                                                                                                    27.7%; Score 445.5; DB 2;
41.7%; Pred. No. 4.6e-25;
iive 31; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
T42405
Bax-3 protein - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPQPN----LHWR 270
                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 91; Conserv
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11; 82 27 AQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPT--IRWLLNGQPL--SMVPPDPHHLL | : | | : | | : | | : | | : | | : | | : | : | 41; Length 423; Indels 22.2%; Score 356.5; DB 2; llarity 33.8%; Pred. No. 4.2e-19; Conservative 45; Mismatches 104; A;Map position: X A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3

m

#status predicted

121

99 63

37;

Indels

Length 1898;

173

2

Gaps

42;

Length 1535;

425

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peroxidasin - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Date: 1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
C;Accession: 346224
R;Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke EMBO J. 13, 3438-3447, 1994
A;Title: Peroxidasin: a novel enzyme-matrix protein of Drosophila development.
A;Reference number: 346224; MUID:94341255; PMID:8062820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1535 (ARE)
A;Cross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385
C;Superfamily: peroxidasin; myeloperoxidase homology; proteoglycan amino-terminal homology
F;19-44/Domain: proteoglycan amino-terminal homology <PAH4>
F;661-1350/Domain: myeloperoxidase homology <MPX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 KKGKKVSSQRFEVIEFDD----GAGSVLRIQP-----LRVQRDEAIYECTAINSLG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 LILLQP------NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTAPQSQT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XTYMCVATNSAGHRESRAARVSIQE----PQDYTEPVELLAV---RIQLENVTLLNPDPA 255
F;811-895/Domain: fibronectin type III repeat homology <FN3F>
F;906-990/Domain: fibronectin type III repeat homology <FN3G>
F;1002-1079/Domain: fibronectin type III repeat homology <FN3G>
F;1025-1275/Domain: fibronectin type III repeat homology <FN3H>
F;1252-1275/Domain: fibronectin type III repeat homology <FN3H>
F;1256-1898/Domain: intracellular #status predicted <INT>
F;1286-1898/Domain: intracellular #status predicted <INT>
F;1286-1898/Domain: protein-tyrosine-phosphatase homology <FPPP>
F;155-1878/Domain: protein-tyrosine-phosphatase homology <FPPP>
F;155-1878/Domain: protein-tyrosine-phosphatase homology <FPPP>
F;155-1878/Domain: protein-tyrosine-phosphatase homology <FPPP>
F;117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted F;1836/Binding site: substrate phosphate (Arg) #status predicted F;1836/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 LNGOPLS-----MVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 TAVSRGARLSVAVLRED------FOIOPRDMVAVVGEOFTLECGPPWGHPEPTVSWWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGSLP----LLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGOPPPTIRWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPRDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGKPL--ALOPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFLPVDPASSNGRIKOLRSGALOIESSEESDOGKYECVATNSAGTRYSAPANLYVR 226
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15.7%; Score 253; DB 2; Length 15
Best Local Similarity 30.3%; Pred. No. 8e-11;
Matches 80; Conservative 33; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 253.5; DB 2;
Pred. No. 9.3e-11;
; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::
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Best Local Similarity 31.8
Matches 75; Conservative
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Niconteanns: protein-tycanie-popolatase (EC 3.1.3.48)
Sisterate names: leukocyee common antigen homology
Niconteanns: protein-tycanie-popolatase (EC 3.1.3.48)
Cippercis Astructur norvegicus (Norway and 2016)
Astructur norvegicus (Norway (Norway and 2016)
Astructur norvegicus (Norway (Norway and 2016)
Astructur norvegicus (Norway (Norway (Norway 
                                                                                                             S2 VLDTGSLFLLKVNSGKNGKD----SDAGAYYCVASNEHGEVKSNEGSLKTAMIREDFRV 136
                                                                                                                                                                                                       QPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQP-GRHTV-SGGSLLMARAEK 199
          81
      25 ASNLAPVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWYKDGQPVITNKEQVNSHRI
                                                                                                                                                                                                                                                SDSGTYQCVANNMVGERVSNPARLSVFEKPKFEQEPKDMT------VDVGAAVLFDC
                                                                        LPD-GTLLLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQI
                                                                                                                                                                                                                                                                                                                                      SDEXTYMCVATNSAGHRESRAARVSI-----QEPQDYTBPVELLAVRIQLENVTLLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 DPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 299
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leukocyte antigen-related protein precursor - human
NiAlternate names: leukocyte common antigen homolog
NiAlternate names: leukocyte common antigen homolog
Scortein-tyrosine-phosphatase (EC 3.1.3.48)
C;Grecies: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: 803841; JL0051
C;Accession: N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med 158, 1523-1530, 1988
A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane;1-16/Domain: signal sequence #status predicted <SIG>;17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>;17-1807/Domain: extracellular #status predicted <EXT>;17-99/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AjGene: GDB:PTPRF; LAR
AjCross-references: GDB:120138; OMIM:179590
AjMap position: 1p34-1p34
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1285-1886/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1654-1877/Domain: protein-tyrosine-phosphate (Ass) Estatus predicted
F;14-97,146-197,243-288/Disulfide bonds: #status predicted
F;1538/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1544/Binding site: Cys (phosphocysteine intermediate) #status predicted
F;1829/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1835/Binding site: substrate phosphate (Arg) #status predicted
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1403-489/Domain: fibronectin type III repeat homology <FN3B>
1501-383/Domain: fibronectin type III repeat homology <FN3B>
1504-883/Domain: fibronectin type III repeat homology <FN3D>
1608-798/Domain: fibronectin type III repeat homology <FN3D>
1908-999/Domain: fibronectin type III repeat homology <FN3F>
1908-999/Domain: fibronectin type III repeat homology <FN3F>
11 repe
--GVYRCLAKNPGSARVGNEAEL--RILSESGLHRQQVFLQRPSNVVAIEGQDAVLECAV 263
                                                                                                                                                                 323 ADLTVMVPPQFLNHPANLYAXESMDIEFE-----CAVSGKPSPTV--KWTKNGEVVI 372
                                                                                                                                                                                                                                                                                AARVSIQEPQDYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRL 276
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                                                                                                                       PWGHPEPTVSWWKDGKPLALQPGRHTVSGGS-LLMARAEKSDEXTYMCVATNSAGHRESR
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A;Cross-references: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
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31.3%; Pred. No. 4.3e-10;
tive 41; Mismatches 80
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Status: nucleic acid sequence not shown
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Conservative 4
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Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN 278
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                                                 208
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C;Species: Gallus gallus (chicken)
C;Date: 13.Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: $26180
R;Volkmer, H.; Hassel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
J. Cell Biol. 118, 149-161, 1992
A;Title: Structure of the axonal surface recognition molecule neurofascin and its relating A;Reference number: $26180; MUID:92317154; PMID:1377696
A;Accession: $26180
A;Accession: $26180
A;Accession: $26180
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1272 <VOL>
A;Accoss-references: EMBL:X65224; NID:g63659; PIDN:CAA46330.1; PID:g63660
C;Superfamily: neural cell adhesion molecule Li; fibronectin type III repeat homology; i
F;279-336/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tunces suppressor - African clawed frog
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
CiAccession: 151669
R.Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.
Aritle: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the Areference number: 151669 MUD:95113183; PMID:7813784
Arecession: 151669
Arecession: 151669
Aresidues: preliminary; translated from GB/EMBL/DDBJ
Aresidues: 1-1427 PPIE>
Arecession: CiGenetics: Areferences: EMBL:U10986; NID:9606873; PIDN:AAA70168.1; PID:9606874
Arecession: XDCCa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR----- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 ALLRCEITGEPMPTISWOKNEEDLKVTPGDPRLLVLPSGTLQI----SRLQTADG---- 207
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            Dd-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 PQILVHPQDQLFQGPG-PARMSCRASGQPPFTIRWLLNGQPLSMVPPDPHHLLPDGTLLL
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        GVYRCTAHNENG-ETSVEATIKVERSQSPPQLAIEPSNLVAITGTTIEL-
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15.2*; Score 245; DB 2; Length 142
Best Local Similarity 31.0*; Pred. No. 2.9e-10;
Matches 75; Conservative 32; Mismatches 99; Indels
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                                                                                      256 EGPKPRPAVWLXWKVSGPXRLPNL 279
                                                                                                                                    SADQPEDGLQISWRHDGRLIDPNV 602
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Best Local Simi
Matches 71;
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protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N.Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: S46217; S51174; Ā49104
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem, J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
A;Reference number: S46216; MUID:94347119; PMID:8068021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1788, 'G',1730-1863 <GOL>
A; Residues: 1-1788, 'G',1730-1863 <GOL>
A; Residues: 1-1788, 'G',1730-1863 <GOL>
A; Croserset errences: EMBL:111587, NID:9205134; PIDN:AAC37656.1; PID:9205135
A; Crosersenan, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silvenn J. Biol. Chem. 268, 24880-24886, 1993
A; Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ner A; Reference number: A49104; MUID:94043351; PMID:8227050
A; Recession: A49104
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Molecule: 1-596,'R', 598-603,'I', 967-1788,'G', 1790-1863 <YAN>
A; Residues: 1-596,'R', 598-603,'I', 967-1788,'G', 1790-1863 <YAN>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:139669)
C: Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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14.8%; Score 237:5; DB 2;
Best Local Similarity 30.9%; Pred. No. 1.4e-09;
Matches 72; Conservative 40; Mismatches 82;
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submitted to the EMBL Data Library, February 1993
A;Reference number: S51174
A;Accession: S51174
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A,Residues: 1-1863 <ZHA>
A,Cross-references: EMBL:L11587
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C;Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change 20-Jun-2000
C;Casesion: 158148; S46218
C;Accasion: 158148; S46218
C;Accasion: 158148; S46218
A;Title: A noval receptor-type protein tyrosine phosphatase is expressed during neuroger A;Title: A noval receptor-type protein tyrosine phosphatase is expressed during neuroger A;Title: A noval receptor-type protein tyrosine phosphatase is expressed during neuroger A;Title: A noval receptor-type protein tyrosine phosphatase is expressed during neuroger A;Title: A noval receptor-type protein tyrosine phosphatase is expressed during neuroger A;Reference number: 158148
A;Rocasion: 158148
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A;Rocasion: 546216; MUID:94347119; PMID:8068021
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                                                                                                                                                            62 KVSSQRFEVIEFDD----GAGSVLRIQP-----LRVQRDEAIYECTATNSLG-EIN 107
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence
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                                                                                                                                                                                                                                                                          A;Status; preliminary
A;Status; preliminary
A;Status; preliminary
A;Status; preliminary
A;Rolecule type: mRNA
A;Residues: 1-1907 veNAG>
A;Cross-references: EMBL:X82288; NID:9587483; PIDN:CAAS7732.1; PID:9587484
A;Redeldues: 1-1907 veNAG>
A;Cross-references: EMBL:X82288; NID:9587483; PIDN:CAAS7732.1; PID:9587484
B;Hendriks, W; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Reference number: S40280
A;Reference number: S40280
A;Recession: S40281
A;Residues: 1441-1501, E',1503-1546 vHEN>
A;Residues: 1441-1501, E',1503-1546 vHEN>
A;Residues: H4H-1501, E',1503-1546 vHEN>
A;Cross-references: EMBL:Z23050; NID:9438137; PIDN:CAA80585.1; PID:9438138
A;Cross-references: EMBL:Z23050; NID:9438137; PIDN:CAA80585.1; PID:9438138
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology vINM1>
F;246-300/Domain: immunoglobulin homology vINM2>
F;4413-506/Domain: immunoglobulin homology vINM2>
F;1375-1596/Domain: protein-tyrosine-phosphatase homology vPPP2>
F;1375-1596/Domain: protein-tyrosine-phosphatase homology vPPP2>
F;1544/Binding site: substrate phosphate (AR9) #status predicted
F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1845/Binding site: substrate phosphate (Arg) #status predicted
F;1845/Binding site: substrate phosphate (Arg) #status predicted
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A14695
axonal glycoprotein TAG-1 precursor - rat
c;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 21-Jan-2000
C;Accession: A34695
R;Furley, A.J.; Morton, S.B.; Manalo, D.; Karagogeos, D.; Dodd, J.; Jessell, T.M.
Cell 61, 157-170, 1990
A;Title: The axonal glycoprotein TAG-1 is an immunoglobulin superfamily member with neur
A;Reference number: A34695; MUID:90199890; PMID:2317872
A;Accession: A34695
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-1040 <FUR>
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C; Accession. 550893; Borboom, D.; Tremblay, M.L.
Bur. J. Biochem. 226, 773-782, 1994
A; Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type A; Reference number: S50893; MUID:95112841; PMID:7529177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 NSORFETIDFDE----SSGAVLRIOP-----LRTPRDENVYECVAONSVG-EIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 RGARLSVAVLREDFQIQPRDMVAVVGEQF-----TLECGPPWGHPEPTVSWWKDGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 IHAKLT--VLRED-QLPPGFPNIDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GSLPLLLLLINGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRW-----LL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82; Indels 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.9
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
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A;Cross-references: EMBL:X68274; NID:g36674; PIDN:CAA48335.1; PID:g36675
R;Hasler, T.H.; Rader, C.; Stoeckli, E.T.; Zuellig, R.A.; Sonderegger, P.
Bur, J. Biochem. 211, 329-339, 1993
A;Title: cDNA cloning, structural features, and eucaryotic expression of human TAG-1/axo
A;Reference number: S28830; MUID:93145965; PMID:8425542
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A;Map position: 1q32-1q32
C;Superfemily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Superfemily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Reywords: cell adhesion; glycoprotein
F;128/Domain: signal sequence #status predicted <SIG>F;128/Domain: signal sequence #status predicted <SIG>F;251-1040/Product: axonal glycoprotein TAG-1 #status predicted <AMT>F;254-308/Domain: immunoglobulin homology <IMM1>F;341-397/Domain: immunoglobulin homology <IMM2>F;76,198,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (coval
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A.Title: Isolation of the cDNA and chromosomal localization of the gene (TAX1) encoding
A;Cross-references: GB:M31725; NID:g207148; PIDN:AAA42201.1; PID:g207149
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: glycoprotein
F;343-399/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 SPPATYRWKKMNGTDMNLEPGSRHQLM-GGNLVIMSP-----TKTQDAGVYQCLAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRLGTAVSRGARLSVAVLREDFQIQPRDMVAV-VGEQFTLECGPPWGHPEPTVSWWKDGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAL-QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSI- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 PNFIPTDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFSTKSVFSKFAQLNLA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LILLVLATVALVSSPGWSFÄQGTPATFGPIFEEQPIGLLFPEE---SAEDQVTLACRARA 67
                                                                                                                                                                                                                                                                                                                                                                                                    18 LLLLIMG------GMAQDSP-----PQILVHPQDQLFQGPGPARMSCRASG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QEPQDYT-----EPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 71; Gaps
                                                                                                                                                                                                                          Length 1040;
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                                                                                                                                                                                                                      Query Match 14.7%; Score 236.5; DB 2; Best Local Similarity 28.2%; Pred. No. 8.7e-10; Matches 84; Conservative 43; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transient axonal glycoprotein TAG-1 precursor - human
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'ubmitted to the EMBL Data Library, September 1992
',Reference number: S35508
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                                                                                                                                                                      123 AVSRGARLSVAVLREDFQIQPRDMY-AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL- 180
                                                                                                                                                                                                                                                       120 VVSREAILRFGFLQE-FSKEERDPVKAHEGWGVMLPCNPPAHYPGLSYRWLLNEFPNFIP 178
                                                           3 SGGDSLIGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGOPPPT 62
                                                                                      23 SAWSSALGSQTT------FGPVFEDQPLSVL-FPEBSTEB---QVLLACRARASPPAT 70
Best Local Similarity 28.7%; Pred. No. 1.9e-09;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       227 ----EPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272
                                                                                                                                                                                                                                                                                                                                                                                                                     : : | | : : | | : : | | 236 LPAPSIKARPPAETYALVGQQVTLECPAFGNPVPR------IKWRKVDG 278
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GenCore version
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OM protein - protein search, using sw model

January 30, 2004, 15:45:39 ; Search time 10.4663 Seconds (without alignments) 1361.423 Million cell updates/sec Run on:

US-10-047-021-86 Perfect score:

1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGORRNTG 303 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P10586 homo sapien	rattu	Q02246 homo sapien	mus m	P23468 homo sapien	mus n	P16621 drosophila	P97603 rattus norv	homo	homo 8	gallı	gallus	mus mu	drose	homo	рошо	mus n		gall	caenor		homo 8		P11627 mus musculu	Q9bmn8 caenorhabdi		P32004 homo sapien		P13595 mus musculu		-		P14781 gallus gall
SUMMARIES	QI	TPF	AXO1_RAT	AXO1 HUMAN	PGBM MOUSE		NEO1 MOUSE					NEO1_CHICK	AXO1 CHICK	DCC_MOUSE	NRG_DROME	DCC_HUMAN	PGBM HUMAN	NCM2 MOUSE		NCA1 CHICK	UN89_CAEEL	NRCA_CHICK	NCM2_HUMAN	NGCA_CHICK	CAML_MOUSE	LAR_CAEEL	RAGE_BOVIN	CAML HUMAN	NCA2_MOUSE	NCA1_MOUSE	AMAL_DROME	1 1	UN52_CAEEL	CONT_CHICK
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de	Query	5	14.7	14.4	14.4	٠	13.9	٠						13.0								12.1		•	٠	11.7	٠	٠	11.5	٠	٠	11.4	11.4	11.4
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P13596 rattus norv 005695 rattus norv 060469 homo sapten P31836 bos taurus P34082 drosophila P13591 homo sapten Q15109 homo sapten Q280198 rattus norv Q28730 oryctolagus P12960 mus musculu
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183 182 179 174.5 173.5 173.5 173.5 170.5 168 167.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90046860; PubMed=2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
"A family of receptor-linked protein tyrosine phosphatases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90316093; PubMed=1695146; Streuli M., Saito H.; Streuli M., Krueger N.X., Thai T., Tang M., Saito H.; Inclient Inclied of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PTFASE).
FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 9:2399-2407(1990).
-1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                  Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.; "A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen."; J. Exp. Med. 168:1523-1530(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-JUL-1989 (Rel. 11, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48)
PTPRF OR LAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989)
   PRT; 1897 AA.
                                                                                                                                                                                                                                                     MEDLINE=89035978; PubMed=2972792;
                                   Created)
 STANDARD;
                                                                                                                            Homo sapiens (Human)
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MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 PLS-----MVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RGARLSVAVLREDFQIQPRDMVAVVGEQF-----TLECGPPWGHPEPTVSWWKDGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S03841; TDHULK.

BDB; 1LARY, 25-APR-00.

Genew; HGNC:9670; PTPRF.

MIM; 179590; ...

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. ..; TAS.

GO; GO:0007125; P:call adheaion; TAS.

GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. ..; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LPLLLLLIMGGMAQ----DSPPQILVHPQDQLFQGFGFARMSCRASGQPPFTIRWLLNGQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VPLVPALVMLGLVAGAHGDSKPVFIKVPEDQTGLSGGVASFVCQATGEPKPRITWMKKGK
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BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
C-SS: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                               R InterPro; IPR003962; FLII subd.
R InterPro; IPR003962; FNIII subd.
R InterPro; IPR003962; FNIII subd.
R InterPro; IPR003962; FNIII subd.
R InterPro; IPR003006; Ig_dike.
R InterPro; IPR003006; Ig_dike.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR000387; TYr_PP.
R Flam; PF00041; Fn3; 7.
R Ffam; PF00041; fn3; 7.
R Ffam; PF000102; Y_Dhosphatase; 2.
R RINTS; PR000102; Y_Dhosphatase; 2.
R RINTS; PR000109; RNTYPEIII.
R SWART; SW00060; FN3; 4.
SWART; SW00060; FN3; 4.
R SWART; SW00060; FN3; 4.
R ROSITE; PS50083; TYR_PHOSPHATASE 1; 2.
R RPGSITE; PS50055; TYR_PHOSPHATASE—PTP; 2.
R PROSITE; PS50055; TYR_PHOSPHATASE—PTP; 2.
R Hydrolase; Receptor; Glycoprotein; Repeat; 3D-structure.
R CANNAT I mmunoglobulin domain; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 244.5; DB 1; Length 1897; 31.3%; Pred. No. 1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPIASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1897 AA; 211844 MW; 439850F1D5C031FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             LAR PROTEIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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            EMBL; Y00815; CAA68754.1;
PIR; S03841; TDHULK.
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Matches 73; Conservative
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1829
107
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SEQUENCE
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DOMAIN
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ACT_SITE
CARBOHYD
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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9019980; PubMed=2317872;

Rurley A.J., Morton S.B., Manalo D., Karagogeos D., Dodd J.,

A. Jessell T.M.;

Basell T.M.;

"The axonal glycoprotein TAG-1 is an immunoglobulin superfamily
member with neurite outgrowth-promoting activity.";

Cell 61:157-170(1990).

Cell 61:170(1990).

Cell 61:170(1990).

Cell 61:170(1990).

Cell 61:170(1990).

Cell 61:170(1990)
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTACTIN WATURE FORM (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)
(Transient axonal glycoprotein 1) (TAX-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R InterPro; PR003961; FN III.
R InterPro; PR003061; Ig-InterPro; PR0030061; Ig-InterPro; PR0030061; Ig-InterPro; PR0030061; Ig-InterPro; PR000041; InterPro; IR Pfan; PR000041; InterPro; PR000041; FNTYPEIII.
R SWART; SW00060; FN3; 4.
R SWART
PRT; 1040 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 31-41.
TISSUE=Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M31725; AAA42201.1; -.
                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
1015
1040
130
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                          CNTN2 OR TAX1
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CARBOHYD
CARBOHYD
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SOLITIES SELECTED SEL
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                                                                                                                                                                                                                                                                                                                                                                                                                     NRIGTAVSRGARISVAVIREDFQIQPRDMVAV-VGEQFTLECGPPWGHPEPTVSWWKDGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 NPVGTVVSKEAVLRFGFLQE-FSKEERDPVKTHEGWGVMLPCNPPAHYPGLSYRWLLNEF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLAL-QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSI- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLLIMG-----GMAQDSP-----PQILVHPQDQLFQGPGPARMSCRASG 57
                                                                                                                                                                                                                                                                                                          LLLLVLATVALVSSPGWSFAQCTPATFGPIFEEQPIGLLFPEE---SAEDQVTLACRARA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QEPQDYT-----EPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AEDPRLFAPSIKARFPPETYALVGQQVTLECFAFGNPVPR------IKWRKVDG 280
                                                                                                                                                                                                                                     71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=93145965; PubMed=8425542;
Hasler T.H., Rader C., Stoeckli E.T., Zuellig R.A., Sonderegger P.;
"CDNA cloning, structural features, and eucaryotic expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=96163865; PubMed=8586412;
Kozlov S.V., Giger R.J., Hasler T., Korvatska B., Schorderet D.F.,
Sonderegger P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsiotra C.P., Karagogoos D., Theodorakis K., Michaelidis M.T., Modi W.S., Furley J.A., Jessel M.T., Papamatheakis J.; Isolation of the cDNA and chromosomal localization of the gene (TAX1) encoding the human axonal glycoprotein TAG-1."; Genomics 18:562-567(1993).
   (POTENTIAL)
                                                                                                                                                                                             ; Score 236.5; DB 1; Length 1040; Pred. No. 2.1e-10; 43; Mismatches 100; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3

AXO1 HUMAN

ID AXO1 HUMAN

AC 002246; P78432;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)

DE (Transient axonal glycoprotein 1) (TAX-1).

GNTN2 OR TAXI OR TAGI.
                                                                                                                                                             MW; 6E707EF6614CB4FB
 GLCNAC.
N-LINKED
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                                                                                                                                                                                                 14.78;
                                                                                                                                                               113042
                                                                                                                                                                                                                  28.28;
                                                                                                                                                                                                                  Similarity 28.2 84.7 Conservative
 206
4463
4463
527
777
920
920
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 206
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SEQUENCE
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Best Local 9
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                                                                                                                                                                                 TISSUE=Placenta;
Taiscura (P., Theodorakis C., Michaelidis M.T., Mamalaki C.,
Taiscura (P., Theodorakis J.; Michaelidis M.T., Mamalaki C.,
Karagogeus D., Papamatheakis J.; Cenbank/DDBJ databases.
L. FUNCTION: MAY PLAY A ROLE IN THE INITIAL GROWTH AND GUIDANCE OF
AKONS. MAY BE INVOLVED IN CELL ADHESION.
L. SUBCELLULAR LOCATION: ATTACHED TO THE NEURONSL MEMBRANE BY A
GPI-ANCHOR AND IS ALSO RELEASED FROM NEURONS.
L. SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
L. SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMOUED IN MATURE FORM (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C3-TYPE 6.
IG-LIKE C3-TYPE 7.
IG-LIKE 7.
IG-LIKE C3-TYPE 7.
IG-LIKE C3-TYPE 7.
IG-LIKE C3-TYPE 7.
IG-LIKE 7.

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(POTENTIAL).
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(POTENTIAL).
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                        molecule TAG-1/axonin-1: genomic structure and basic promoter.",
Genomics 30:141-148(1995).
The human TAX1 gene encoding the axon-associated cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 76 N-LINKED (GLCNAC...) (POTENT 204 198 198 N-LINKED (GLCNAC...) (POTENT 461 461 N-LINKED (GLCNAC...) (POTENT 477 477 N-LINKED (GLCNAC...) (POTENT 498 498 N-LINKED (GLCNAC...) (POTENT 525 525 N-LINKED (GLCNAC...) (POTENT 830 830 N-LINKED (GLCNAC...) (POTENT 918 918 N-LINKED (GLCNAC...) (POTENT 940 N-LINKED (GLCNAC...) (POTENT 1012 1012 GP1-ANCHOR (POTENTIAL)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000041; fn3; 4.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 3.
SMART; SM00408; IG_LIKE; 6.
Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor; Cell adhesion; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 190197; -.
Oct. Go;0005867; C:integral to plasma membrane; TAS. InterPro; IPR003961; FN III.
InterPro; IPR003962; PnIII.
InterPro; IPR007110; Ig-11Ke.
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EMBL; X67734; CAA49963.1; -.
EMBL; X92681; CAA63365.1; -.
EMBL; X84420; CAA59137.1; -.
PIR; S35508; A49356.
HSSP; P40189; 1BQU.
                                                                                                                                                        SEQUENCE OF 1-136 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:2172; CNTN2.
MIM; 190197; -.
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1012
1040
128
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LIPID
SEQUENCE
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CARBOHYD
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EMBL, M77174; AAA39911.1; -.
EMBL, J04054; AAA3899.1; -.
EMBL, J04055; AAA39912.1; -.
PDR; S18252; S18252.
PDB; IGL4; 28-NOV-01.
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14;
                                                                                                                                               71 YRWKMNGTEMKLEPGSRHQLV-GGNLVIMNP-----TKAQDAGVYQCLASNPVGT 119
                                                                                                                                                                         123 AVSRGARLSVAVLREDFQIQPRDMV-AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL- 180
                                                                                                                                                                                        120 VVSREAILRFGFIQE-FSKEERDPVKAHEGMGVMLPCNPPAHYPGLSYRWLLNBFPNFIP 178
                                                                                                                                                                                                                           181 OPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSIQ---- 226
                                                                                                                                                                                                                                          63 IRWLLNGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGT 122
                                                                  SGGDSLLGGRGSLPLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPT 62
                                                                                           SAWSSALGSQTT-----FGPVFEDQPLSVL-FPEESTEE---QVLLACRARASPPAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89034110; PubMed=2972708; MEDLINE=89034110; PubMed=2972708; MEDLINE=89034110; PubMed=2972708; Moonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M., Nordan D.M., Hassell J.R., Ledbetter S.R., Vogeli G., Sasaki M., "Identification of cDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan."; J. Biol. Chem. 263:161379-16387(1988).

-!-FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.

-!-SUBGNAT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M., Yanada Y., Hassell J.R., Valente P., Cai S., Horigan E., Sasaki M., Yamada Y., Hassell J.R., Perlecan, a basement membrane heparan "The complete sequence of perlecan, a basement membrane heparan cultate protecoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane components such as laminin, prolargin and collagen type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
PTM: CONTAINS THREE HEPRAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: Contains 4 LDL-receptor class A domains.
SIMILARITY: Contains 11 laminin EGF-like domains.
                                                                                                                                                                                                                                                                               227 -----EPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                      603
           14.4%; Score 232; DB 1; Length 1040; 28.7%; Pred. No. 4.6e-10; ive 41; Mismatches 108; Indels 60
                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
Protein precursor (HSPG) (Perlecan) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 266:22939-22947(1991)
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                                       84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                          Similarity
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Q05793;
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-- PWQHRIEGNTLVIPRVAQQDSGQYICNATNSAGHTEATVV-LHVESPPYATIIPEHTS 2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 ----VSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οţ
                                                                                                                                                                                                                                                                                                                                                            2519 VELIVDTG---TVAPGTPQVQVEESELTLEAGHTATLHCSAT-GNPPPTIHWSKLRAPL-
                                                                                                                                                                                                                                                                                                                                 GMAQD-----SPPQILVHPQDQLFQGPGPARM----SCRASGQPPTIRWLLNGQP
                                                                                                                                                                                                                                                                                                                                                                                                                          72 LSMVP----PDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LOPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPODYT----
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=11006018; PubMed=2170109;
Krueger N.X., Streuli M., Saito H.;
Structural diversity and evolution of human receptor-like protein
"Structural diversity and evolution of human receptor-like protein
tyrosine phosphateses.";
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
-!- CATENATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
MEDLINE=95204468; PubMed=7896816;
MEDLINE=95204468; PubMed=7896816;
Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
"Molecular characterization of the human transmembrane protein-
tyrosine phosphatase delta. Evidence for tissue-specific expression
alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPTPD HUMAN STANDARD; PRT; 1912 AA.
P22468;
01-NOV-1991 (Rel. 20, Created)
10-CCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-delta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1015_TaxID=9606;
                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                   Length 3707;
                                                                                                                                                                                                                                                                                  88; Indels
                                                                                                                                                                                                                                      DB 1;
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Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2631 AQPGNL----VQLQCL-----AHGTPPLTYQW 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 -EPVELLAVRIQLENVTLLNPDPAEGPKPRPAVW 265
                                                                                                                                                                                                                                   231.5; DB
No. 2e-09;
                                                                                                                                                                                                                    14.4%; Scc. No. 2.27.7%; Pred. No. 2.1.37; Mismatches
                   SIMILARITY.
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J. Biol. Chem. 270:6722-6728(1995)
SEQUENCE OF 390-1912 FROM N.A. TISSUE=Placenta;
                                                                                                                                                                                                                                                                                  76; Conservative
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15;

73 99

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L--ALQPGR-----HTVSG----GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 VDTSNNNGRIKQLRSESIGGTPIRGALQIEQSEESDQGKYECVATNSAGTRYSAPANLYV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----MVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALST--DLGVYTCEASNRLGTAVSRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 ORFEVIEFDD----GSGSVLRIQP-----LRTPRDEAIYECVASNNVG-EISVS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ARLSVAVLREDFQIQPRDMVAV-VGEQF-----TLECGPPWGHPEPTVSWWKDGKP 177
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.3%; Score 230; DB 1; Length 1912; Best Local Similarity 33.1%; Pred. No. 1.3e-09; Matches 80; Conservative 38; Mismatches 72; Indels 52; Gaps
                                                                                                                                                                                                                                                                                                                                                          17 LLLLLIMGGMAQD--SPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRWLLNGQPLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                          R->A: 2.5-FOLD REDUCTION IN CLEAVAGE. W; 3AE8CBCD32182E26 CRC64;
    (POTENTIAL) (POTENTIAL)
                                                                                 Missing (In isoform 2).
/FTId=VSP 005148.
Missing (In isoform 2).
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                         (in isoform 2)
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      (GLCNAC.
                                                                005147
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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IsoId=P97798-1; Sequence=Displayed;
    N-LINKED (N-LINKED (Missing (i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=97407661; PubMed=9264410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
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NEO1 OR NGN.
      724
832
181
                                                                                                                              775
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    CARBOHYD
CARBOHYD
VARSPLIC
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                                                                                      /ARSPLIC
                                                                                                                              VARSPLIC
                                                                                                                                                                   VARSPLIC
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NEO1 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. .; TAS.
IsoId=P23468-1; Sequence=Displayed;
Name=2; Synonyms=Kidney;
IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
IsoId=P23468-3; Sequence=VSP_005150;
Name=3; Synonyms=Fetal brain;
IsoId=P23468-3; Sequence=VSP_005150;
PTM: A CLEAVKGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN FROM THE TRANSMEMBRANE SEGMENT.
SIMILARITY: COntains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE PTP; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat; Immunoglobulin domain; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PROTEIN-TYROSINE PHOSPHATASE DELTA.
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IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 6.

FIBRONECTIN TYPE-III 6.

FIBRONECTIN TYPE-III 6.
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N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003961; FN_III.
Interpro; IPR003961; FN_III.
Interpro; IPR003962; FnIII subd.
Interpro; IPR003998; Ig-1ike.
Interpro; IPR003109; Ig_MHC.
Interpro; IPR000387; TYR_phosphatase.
Interpro; IPR000387; TYR_phosphatase.
Interpro; IPR000242; Tyr_PP.
Pfam; PF00104; Fn3; 8.
Pfam; PF00104; ig; 3.
Pfam; PF00104; ENYPEIII.
PRINTS; PR00104; PWYYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L38929; AAC41749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X54133; CAA38068.1; -. PIR; A56178; A56178. HSSP; P18052; 1YFO. Genew; HGNC:9668; PTPRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00060; FN3; 8.
SMART; SM00408; IGC2; 2.
SMART; SM00194; PTPC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 601598; -.
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DOMAIN
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1493 AA; 163159
                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                 229 QDYTEPVELL 238
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                               1096
                                                     1331
            878
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                                1086
                                                     1279
            863
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            VARSPLIC
                                                                          SEQUENCE
                                                                                              Query Match
                                VARSPLIC
                                                     VARSPLIC
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                                                  ISOId=P97798-5; Sequence=VSP 002597;
Note=Expression developmentally regulated;
Note=Expression developmentally regulated;
TISSUE SPECIFICITY: Widely expressed.
DEVELOPMENTAL STAGE: EXPRESSED UBIQUITOUSLY THROUGHOUT THE MID TO LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE EIS. 5 MOUSE NEURAL TUBE, AS IN THE VENTRICULAR ZONES OF THE MESENCEPHALON AND RHOMBENCEPHALON. ISOPORMS 3 AND 4 ARE EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN B11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; smoveco, ..... ICE. LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain; Glycoprotein; Alternative splicing.
Clycoprotein; Alternative splicing.
POTENTIAL.
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(POTENTIAL)
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                                                                                                                                                                       SUBFAMILY.
SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                               SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

G-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 4.

PIBRONECTIN TYPE-III 1.

PIBRONECTIN TYPE-III 2.

PIBRONECTIN TYPE-III 3.

PIBRONECTIN TYPE-III 3.

PIBRONECTIN TYPE-III 4.

PIBRONECTIN TYPE-III 4.

PIBRONECTIN TYPE-III 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 2)
                      Sequence=VSP 002596;
developmentally regulated;
 Note=Expression developmentally regulated,
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(GLCNAC.
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N-LINKED (GLCWA
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InterPro; IPR003962; FNIII subd.
InterPro; IPR003100; Ig-11ke.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003066; Ig_MHC.
Pfam; PP00041; fn3; 6.
Pfam; PP00047; ig; 4.
PRINTS; PR00014; FNTYPEIII.
SNART; SN00666; FN3; 6.
                                                                                                                                                                                                                                                                                                      EMBL; Y09535; CAA70727.1; -.
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11136
11157
1493
249
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MGI:1097159; Neol.
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1153
140
232
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421
84
221
337
501
520
670
        Name=4;
IsoId=P97798-4;
Note=Expression
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DOMAIN
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CARBOHYD
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89 SEPSPNIEWKKDGTFLNLESDDRRQLLPDGSLPISNVVHSKHN-----KPDEGFYQCVA 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194
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SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 LPLLLLGRPASGAAATKSGPRROSOGASVRTFTPFYFLVEPVDTLSVRGSSVILNCSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 SWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSI-QEP
                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LPLLLLL---IMGGMAQDSPPQ------ILVHPQDQLFQGPGPARMSCRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 GOPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. TP POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASS). IT CONTROLS MOTOR AXON GUIDANCE. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.; "A family of receptor-linked protein tyrosine phosphatases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase) (dLAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-S;
MadblinE=96178473; PubMed=8598047;
Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,
Saito H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The transmembrane tyrosine phosphatase DLAR controls motor axon guidance in Drosophila.";
Cell 84:611-622(1996).
                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                13.9%; Score 223; DB 1; Length 1493; 29.6%; Pred. No. 3.3e-09; tive 32; Mismatches 104; Indels 40
                           Missing (In isoform 3).
/FIId=VSP 002595.
Missing (In isoform 4).
/FIId=VSP 002596.
Missing (In isoform 5).
/FIId=VSP 002597.
9 MW, 441DE919D5E17COE CRC64;
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/FTId=VSP 002594
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01-AUG-1990 (Rel. 15, Last seq
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251 NPDP 254
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SEQUENCE
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SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 9 fibronectin type III domains. SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                      R InterPro; IPR003961; FN III.

R InterPro; IPR003106; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003004; TYR_Phosphatase.

R Ffam; PF000041; fn3; 9.

R Pfam; PF00102; Y_Dhosphatase; 2.

R RMNTS; PR00102; Y_Dhosphatase; 2.

R RMNTS; PR00104; FNTYPEIII.

R RMNT; SM00060; RNY; 9.

R SMART; SM000194; PNTPC; 2.

R RNART; SM00194; PNTPC; 2.

R RNOSITE; PS50083; TYR_PHOSPHATASE 1; 2.

R PROSITE; PS50055; TYR_PHOSPHATASE 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-III 9.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                   GO; GO:0008045; P:motor axon guidance; IMP.
GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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BY SIMILARITY
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                                                                                                                                                                         1 U36857; AAC47002.1; -
1 U36849; AAC47002.1; JOINED.
1 U36850; AAC47002.1; JOINED.
1 U36851; AAC47002.1; JOINED.
1 U36852; AAC47002.1; JOINED.
1 U36854; AAC47002.1; JOINED.
1 U36855; AAC47002.1; JOINED.
1 U36855; AAC47002.1; JOINED.
1 U36856; AAC47002.1; JOINED.
                                                                                                                                                             EMBL; M27700; AAA28668.1; -.
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HSSP; P28827; IRPM.
FlyBase; FBgn0000464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDDQGKYECVAENSMGTEHSKATNLYVKVRRVPPTFSRPPETISEVMLGSNLNLSCIAVG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSV------AVLRED 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 FQIQPRDMVAVVGEQFTLECGPFWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 KSDEXTYMCVATNSAGHRESRAARVSI---QEPQDYTEPVE-----LLAVRIQLENVTLL 250
                                                                                                                                                                                                                                                                                                                                                                                                 31 PPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLL--PDGTL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                              PPEIIRKPONGGVRVGGVASFYCAARGDPPPSIVWRKNGKKVSGT-QSRYTVLEQPGGIS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                     34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.-Y., Culotti J.G., Tessier-Lavigne M.;
Culotti J.G., Tessier-Lavigne M.;
Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
Cell 87:175-185(1996)
-!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.-!- SUBCELLULAR LOCATION: Type I membrane protein.
                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 4 immunoglobulin-like C2-type domains. SIMILARITY: Contains 6 fibronectin type III domains.
(POTENTIAL)
                                                                                                                                                                                                                                                                                                          DB 1; Length 2029;
                                                                                                                                                                                                                                                                                                     13.8%; Score 222; DB 1; Length 20:
27.5%; Pred. No. 5.5e-09;
.ive 39; Mismatches 104; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                        N-LINKED
N-LINKED
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Best Local Similarity 27.55
Matches 67; Conservative
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   and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 REDFQIQPRDMVAVVGEQFTLECGPPWGHPE-----PTVSWWXDGKPLALQPGRHTVSG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PR-FTSQPEPSSIYVGNSGILNC-----BVNADLVPFVFWFWEQNRQPLLLDDRIVKLPS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSI-QEPQDYTEPVELL--AVRIQLEN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 SPPQ------ILVHPQDQLFQGPGPARMSCRASGQPPFTIRWLLNGQPLSMVP 76
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                                                                                                                                                        PRINTS, PRO0014; FNTYPEIII.
SWART; SM00060; FN3; 6.
SWART; SM00408; IGC2; 3.
PROSITE; PSS0835; IG LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
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(ODTENTIAL)
(ODTENTIAL)
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N-LINKED (GLCNAC. .) (POTENTIAL)
MW; E514EDBABD1A63A9 CRC64;
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   Usage by
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                       IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
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(GLCNAC. . .)
(GLCNAC. . .)
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or send an email to license@isb-sib.ch).
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                                                                     InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR003110; Ig-11Ke.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003065; Ig_MHC.
Pfam; PF00041; fn3; 6.
Pfam; PF00047; ig; 4.
                                              EMBL; U68726; AAB41100.1; -. HSSP; P56276; 1TLK.
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nes 76, Conservative
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1377 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE PROGRESSION MARKER.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.
C. ILSUB SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
C. ILSUB SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
C. GLAND, OVARY, BRAIN, HEART AND SKELETAM MUSCLE. ALSO EXPRESSED IN EXPRESSED IN COLON.
C. STMILARITY: BELONGS TO THE TYR PAMILY OF PROTEIN KINASES. INSULIN RECEPTION.
                                                                                                                                                                                                                                                                                                                                                                                Ullrich A.;
                                                            30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fibroblast;
MEDLINE=97037064; PubMed=8882711;
Park S.-K., Lee H.-S., Lee S.-T.;
Characterization of the human full-length PTK7 cDNA encoding a receptor protein tyrosine kinase-like molecule closely related to chick KLG.";
                                                                                                                                                                         PTK7 OR CCK4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  TISSUE=colon carcinoma, and Placenta;
MEDLINE=56074849; PubMed=7479540;
MOSBIC K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A
"Colon carcinoma kinase-4 defines a new subclass of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                       PRT; 1070 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL, AF447176; AAL39062.1; -... EMEL, AF447157; AAL39062.1; JOINED. EMEL, AF447157; AAL39062.1; JOINED. EMEL, AF447162; AAL39062.1; JOINED. EMEL, AF447167; AAL39062.1; JOINED. EMEL, AF447170; AAL39062.1; JOINED. EMEL, AF447171; AAL39062.1; JOINED. EMEL, AF447174; AAL39062.1; JOINED. EMEL, AF447174; AAL39062.1; JOINED. EMEL, AF447174; AAL39062.1; JOINED. EMEL, AF447175; AAL39062.1; JOINED. EMEL, AF477175; AAL39062.1; JOINED. EMEL, AF47775; AAL39062.1; JOINED. EMEL, AF47775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biochem. 119:235-239(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U40271; AAC50484.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 11:2179-2184 (1995).
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                       PTK7_HUMAN
Q13308; Q13417;
PTK7_HUMAN
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279 TVFANGSLLLTQVRPR-----NAGIYRCIGQGQRGPFIILEATLHLAEIEDMPL 327
                                       141 IQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKS
                                                                                                                                                                                                                                                      NEO1 HUMAN STANDARD; PRT; 1461 AA. 092859; 000340; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Neogenin precursor.
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R MIM; 601890; -.

R GO; GO:0005886; C:plasma membrane; TAS.
R GO; GO:0005886; C:plasma membrane; TAS.
R GO; GO:0005888; C:proteoglycan integral to plasma membrane receptor protein tyrosine kin. .; TAS.
R GO; GO:000144; F:transmembrane receptor protein tyrosine kin. .; TAS.
R GO; GO:0001465; P:signal transduction; TAS.
R InterPro; IPR003109; Ig-1ke.
DR InterPro; IPR003098; Ig-2.
DR InterPro; IPR003011; RTKinase.
DR InterPro; IPR00119; Prot_kinase.
DR InterPro; IPR00119; Prot_kinase.
DR Pfam; PR00109; TYRKINASE.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD00001; Prot_kinase; 1.
DR PROSTIE; PS00119; PROTEIN KINASE DOM; 1.
DR PROSTIE; PS00119; PROTEIN KINASE TYR; 1.
DR PROSTIE; PS00119; PROTEIN KINASE DOM; 1.
DR PROSTIE; PS00119; PROTEIN KINASE TYR; 1.
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29.2%; Pred. No. 5.9e-09;
Live 35; Mismatches 93; Indels 25; Gaps
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992 992 S -> F (IN REF. 2 AND
1070 AA; 118260 MW; 47CDF25B8E3698A5
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81 HLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ 140 : : | : | | | | : | : 1

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
200
                                    328 FEPR--VFTAGSEERVTCLPPKGLPEPSV-WWEHAGVRLPTHGRVYQKGHELVLANIAES 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
MEDLINE=97312699; PubMed=9169140;
Vielmetter J., Chen X.-N., Miskevich F., Lane R.P., Yamakawa K.,
Korenberg J.R., Dreyer W.J.;
"Molecular characterization of human nebgenin, a DCC-related protein, and the mapping of its gene (NEO1) to chromosomal position 15q22.3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=2;
IsoId=092859-2; Sequence=VSP 002593;
-i- TISSUE SPECIFICITY: WIDELY EXPRESSED AND ALSO IN CANCER CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 41:414-421(1997).

-i- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.
-i- SUBSCELLULAR LOCATION: Type I membrahe protein.
-i- SUBSCELLULAR LOCATION: Type I membrahe protein.
-i- ALTERNATIVE PRODUCTS:
-i- ALTERNATIVE PRODUCTS:
-i- ALTERNATIVE SPAIL STATE STA
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MEDILINE=9723663; PubMed=9121761;
MEDILINE=9723663; PubMed=9121761;
Meyerhardt J., Look A.T., Bigner S.H., Fearon B.R.;
"Identification and characterization of neogenin, a DCC-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
-1- SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                       201 DEXTYMCVATNSAGHRES----RAARVS--IQEPQD 230
                                                                                                                                                                                                         DAGVYTCHAANLAGQRRQDVNITVATVPSWLKKPQD 420
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EXTRACELLULAR (POTENTIAL) POTENTIAL.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUE=Embryonic brain;
MEDLINE=95105243; PubMed=7806578;
                                                                                                                                                                                                                   PRT; 1443 AA
                                                                 258 PKPRPAVWLXWKVSGPXRLPN 278
                                                                                          367 -KPTPTV--KWVKNGDMVIPS 384
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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; Pred. No. 8.3e-09;
40; Mismatches 122; Indels 133; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 GQPPPTIRWLLNGQPLSMVPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 SEPSPKIEWKKDGTFINLVSDDRRQLLPDGSLFISNVVHSKHN-----KPDEGYYQCVA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 TVESLGTIISRTAKLIVAGLPRPTSQPEPSSVYAGNGAILNCEVNADLVPFVRWEQNRQP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 LKÓPSPLVRVIGODVVLPCVAS-GLPTPTIKWMKNEEALDTESSERLVLLAGGSLEISDV 310
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           The GO: GO: GO05887; C: integral to plasma membrane; TAS.

R DiterPro; IPR003961; FN III.

R InterPro; IPR003961; FN III.

R InterPro; IPR003962; FN III.

R InterPro; IPR003006; Ig_d.2.

R InterPro; IPR003006; Ig_MHC.

R Pfam; PF00041; fig. 4.

R RINTS; PR00041; FNTYPEIII.

R PRINTS; PR00041; FNTYPEIII.

R SMART; SM00060; FN3; 6.

RR RNSTTS; RM00060; FN3; 6.

RR PROSTTE; PS50835; IG_LIKE; 4.

RR PROSTTE; PS50835; IG_LIKE; 4.

Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain; M Glycoprotein; Alternative splicing.

T SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 LLLLLLING------GMAQDSPP-----QILVHPQDQLFQGPGPARMSCRAS
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7AAE897E69635A21 CRC64;
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
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/FTId=VSP 002593.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNU
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Best Local Similarity 22.00,
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1105
1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wielmetter J., Roman J.M., Dreyer W.J.;

Wielmetter J., Roman J.M., Dreyer W.J.;

Weogenin, an avian cell surface protein expressed during terminal
neuronal differentiation, is closely related to the human tumor
neuronal differentiation, is closely related to the human tumor
and the coll siol. 127:2009-2020(1994).

J. Cell Biol. 127:2009-2020(1994).

I. FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THERR
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION
MOLECULE IN A BROAD SERCTRUM OF EMBRYONIC AND ADULT TISSUES.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.

C. I. DEVELOPMENTAL STAGE: IN RETINA, EXPRESSED ON GANGLION CELL FIBERS
C. SUBFAMILY:

C. I. SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.

C. I. SIMILARITY: Contains 6 fibronectin type III domains.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
Neogenin (Fragment).
Gallus gallus (Chicken).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E EMBL; U07644; AAC59662.1; -...
R PIR; ISG000; ISO600.
HSSP, P11276; 2MFN.
R INTERPO; IPR003961; FN III.
R INTERPO; IPR003962; FNIII subd.
R INTERPO; IPR003962; FNIII subd.
R INTERPO; IPR003106; Ig_C2.
R INTERPO; IPR0041; FN II.
R PFEM; PF00041; FN II.
R PFEM; PF00041; FN II.
R SMART; SM00060; FN II.
R SMART; SM00408; IGC2; 2.
R PROSITE; PSS0835; IG_LIKE; 4.
R PROSITE; PSS0835; IG_LIKE; 4.
R CG11 adhesion; Repeat; Transmembrane; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ANPPATYRWKMNGTELKM-GPDSRYRLVAGDLVISNP-----VKAKDAGSYQCVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVV---GEQFTLECGPPWGHPEPTVSWWK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGKPLAL-QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LGGRG-----SLPLLLLLI----MGGMAQDSPPQILVHPQDQLF-QGPGPAR--MSCRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Gaps
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                            -1- PIN: The N-terminus is blocked.
-1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-1- SIMILARITY: Contains 4 fibronectin type III domains.
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                         THE NEURONAL MEMBRANE BY
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                                                                                                                                                                                                                                                                                                                                   EMBL, X63101; CAA44815.1; -.
PIR; $22383; $22383.
PDB; 1CS6; 19-MAY-00.
RINCEPPO; IPR007361; FN III.
RINCEPPO; IPR007366; FN III.
RINCEPPO; IPR007366; Ig_c2.
RINCEPPO; IPR003006; Ig_MHC.
REAM, PF00041; Ig; 6.
REAM, PF00047; Ig; 6.
RANRT; $M00060; FN3; 4.
RANRT; $M00408; IGC2; A SMART; SM00408; IGC2.
REAM, PF009111 Gomain; Glycoprotein; Signal; GPI-anchor; Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08B80143BE779794 CRC64;
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REMOVED IN MATURE FORM.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C3-TYPE 6.

IG-LIKE
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N-LINKED
OF NEURITIC MEMBRANE.
SUBCELLULAR LOCATION: ATTACHED TO
GPI-ANCHOR.
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OR 25 (
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223
317
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ses 81; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVR--IQLENVTLLN---PDPAEG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPYRCVIESGGTPKYSEEAELKIL--PDPEEPQSLVFVRQPSSLTKVTGQNAVFPCVAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 VVGEQFTLECGPPWGHPE-----PTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92174898; PubMed=1311675; Zuellig R.A., Rader C., Schroeder A., Kalousek M.B., von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T., Affolter H.-U., Fritz A., Hafen E., Sonderegger P.; Stoeckli E.T., affolter H.-U., Fritz A., Hafen E., Sonderegger P.; Primary structure, immunoglobulin-like and fibronectin-type-III-like domains and sylvosyt-phosphatidylinositol anchorage."; Eur. J. Biochem. 204.453.463(1992).

Eur. J. Biochem. 204.453.463(1992).

FROWOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM II (G4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 215.5; DB 1; Length 1; Pred. No. 1.2e-08; 27; Mismatches 117; Indels
                     | FIBRONECTIN TYPE-111 1. |
| FIBRONECTIN TYPE-111 2. |
| FIBRONECTIN TYPE-111 3. |
| FIBRONECTIN TYPE-111 4. |
| FIBRONECTIN TYPE-111 6. |
| BY SIMILARITY. |
| CALCHAC. | CALCHAC. |
| N-LINKED (GLCNAC. |) (IN-LINKED (GLCNAC. |) (IN-L
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 24, Created)
(Rel. 24, Last seq
(Rel. 42, Last ann
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714
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Best Local Similarity
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SEQUENCE
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P28685;
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166 NEFPNFIPADGRRFVSQTTGNLYIAKTEASDLGNYSCFATS---HIDFITKSVFSKFSQL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fort=1-12; Sequence=-VSP_002501;
Event=Alternative initiation;
Comment=2 isoforms, A (shown here) and B, are produced by
alternative initiation at Met-1 and Met-85;
TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
DEWELOPING BRAIN AND NEUMAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
ISOFORM CIS EXPRESSED ONLY IN THE EMBRYO.
DEWELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
AND REMAIN AT THIS LEVEL IN THE ADULT.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=A;
IsoId=P70211-1; Sequence=Displayed;
Note=Isoform B is produced by alternative initiation at Met-85
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS A, B AND C).
STRATABLABLE O: 11SOSTE=Brain;
STRATABLABLE O: 11SOSTE=Brain;
COOPER H.M., Armes P., Britto J., Gad J., Wilks A.F.;
Cloning of the mouse homologue of the deleted in colorectal cancer
gene (mDCC) and its expression in the developing mouse embryo.";
Oncogene 11:2243-2254(1995).
                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 4 immunoglobulin-like C2-type domains. SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
--I- FUNCTION: IMPLICATED AS A TUNOR SUPPRESSOR GENE.
--I- SUBCELLUIAR LOCATION: Type I membrane protein.
--I- ALTERNATIVE PRODUCTS:
                          SI--QEPQDYTEPVE-----LLAVRIQLENVTLLNPDP 254
                                             |: :: : | | : : 223 SLAAEDARQYAPSIKAKFPADTYALTGOMVTLECFAFGNPVP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                            PRT; 1447 AA
                                                                                                                                                                                              Tumor suppressor protein DCC precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS.
STRAIN=BALB/c; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X85788; CAA59786.1; -. HSSP; P56276; 1TLK.
                                                                                                                            STANDARD;
                                                                                                                                                                                                                        musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:94869; Dcc.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooper H.M.;
Submitted (J
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P70211;
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108 DIGVYTCEASNRLGTAVSRGARLSVAVLRED-----FOIOPRDMVAVVGEOFTLECGP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 PWGHPEPTVSWWKDGKPLALQPGRHTVSGGS-LIMARAEKSDEXTYMCVATNSAGHRESR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AARVSIQEPODYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 AELTVLVPPWFLNHPSNLYAYESMDIEFE-----CAVSGKPVPTV--NWMKNGDVVI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 LKCEVIGEPMPTIHWQKNQQDLNPLPGDSRVVVLPSGALQISRLQP------G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 MSCRASGQPPPTIRWLLNGQPLSMVPPDPH-HLLPDGTLLL--LQPPARGHAHDGQALST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 DSGVYRCSARN--PASIRTGNEAEVRILSDPGLHRQLYFLQRPSNVIAIEGKDAVLECCV
                                                                                                                                                                                ISOFORM A. ISOFORM B.
                                                 PRINTS; PRO0014; FNTYPEIII.
SMART; SMO0006; FN3; 6.
SMART; SMO0408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 4.
Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
Repeat; Anti-oncogene; Alternative initiation; Alternative splicing.
SIGNAL. 1 25 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1447;
                                                                                                                                                                                TUMOR SUPPRESSOR PROTEIN DCC, TUMOR SUPPRESSOR PROTEIN DCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0D1F1097C22D5B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRG DROME STÂNDARD; PRT; 1302 AA. P20241; 061541; 061542; 024414; 024415; 095064; 09903X0; 01-FEB-1991 (Rell. 17, Created) 16-0CT-2001 (Rell. 40, Last sequence update) 15-SEP-2003 (Rell. 42, Last annotation update)
                                                                                                                                                                                                                                                    POTENTIAL.

GYTOPIASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

PIBRONECTIN TYPE-II 1.

FIBRONECTIN TYPE-II 1.
                                                                                                                                                                                                   TUMOR SUPPRESSOR PROTEIN FOR ISOFORM B. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
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BY SIMILARITY.
BY SIMILARITY.
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M-LINKED (GLCNAC.
M-LINKED (GLCNAC.
M-LINKED (GLCNAC.)
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; Pred. No. 3.6e-08;
37; Mismatches 98
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27.7%;
InterPro; IPR003006; Ig_MHC.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E. Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Bauton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ratton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ratandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Man H.D., Andrews-Frankoch C., Baldwin D., Balluw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Bauch S.W., Barman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Bryaktaroglu L., Beasley E.M., Ratis R.C., Busam D.A., Bulke C., Davenport L.B., Davies P., Andrey S., Dankova D., Botchan M.R., Doule C., Ferraz C., Ferriers S., Punkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P., Botshon K.J., Evangelista C.C., Ferraz C., Ferriers S., Punkov B.C., Dunkov B.C., Durbin K.J., Evangelista C.C., Ferraz C., Ferriers S., Punkov B.C., Dunkov B.C., Stanis B.J., Moshrefi A., Gong F., Goriellan A.E., Gary B., Hernandez J.R., Houston B., Molloon K.A., Howlen B.C., Morlas J., Moshrefi A., Balazolo M., Molson K.A., Nixon K., Nussekern D.R., Parl B.C., Siden-Kiamos I., Simpson M., Strong R., Shu B.C., Siden-Kiamos I., Simpson M., Strong R., Sun B., Shilams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Wulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O., Scheeler F., Spradling A.C., Stapleton M., Strong R., Shirk B.D., Smith H.D., Scheeler F., Spradling A.C., Stapleton B.C., Stapleton B.C., Stapleton B.C., Stapleton B.C., Stapleton B.C., Sta
                                                                                                                       SEQUENCE FROM N.A. (ISOFORM SHORT), AND SEQUENCE OF 24-41 AND 737-751. MEDLINE=90030418; PubMed=2805067; Bieber A.J., Snow P.M., Hortsch M., Patel N.H., Jacobs J.R., Traquina Z.R., Schilling J., Goodman C.S.; "Drosophila neuroglian: a member of the immunoglobulin superfamily with extensive homology to the vertebrate neural adhesion molecule
                                                                                                                                                                                                                                                                                                                adhesion
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
BIGDLINE-89332718; PubMed=9666073;
Zhao G., Hortceh M.; Peronic structures in the L1 family of cell adher
"The analysis of genomic structures in the L1 family of cell adher
sproteins provides no evidence for exon shuffling events after the
separation of arthropod and chordate lineages.";
Gene 215:47-55(1998).
                              Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                       Hortsch M.,
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM SHORT). STRAIN-Berkeley; TISSUE-Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
                                                                                                                                                                                                                                   Cell 59:447-460(1989)
 Neuroglian precursor.
                                                                                          NCBI_TaxID=7227;
                 NRG OR CG1634
                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=94213741; PubMed=7512815;
Huber A.H., Wang Y.-M.E., Bieber A.J., Bjorkman P.J.;

Neuron 12:17-711(1994).

-I- FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL
-I- FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL
-I- BURGINAL DISK MORPHOGENESIS. VITAL FOR EMBRYONIC DEVELOPMENT.
-I- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                  SEQUENCE OF 1182-1302 FROM N.A., FUNCTION, ALTERNATIVE SPLICING, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=P20241-2; Sequence=VSP 002601, VSP 002602;
-!- TISSUS SPECIFICITY: LONG ISOFORM IS, RESTRICTED TO SURFACE OF NEURONS AND GLIA IN THE DEVELOPING NERVOUS SYSTEM AND THE SHORT ISOFORM TO OTHER NONNEURONAL TISSUES.
-!- SIMILARITY: BELONGS TO THE IMMUNOSLOBULIN SUPERFAMILY.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90262720; PubMed=1693086;
Hortsch M., Bieber A.J., Patel N.H., Goodman C.S.;
"Differential splicing generates a nervous system-specific form of
Drosophila neuroglian.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; 5.
SMART; SM00408; IGG2; 4.
PROSITE; PS50835; IG LIKE; 6.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; 3D-structure;
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                        Change M., Chavez C., Dorsett V., Farfan D., Frise E., George R. Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Carlson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:000586; C:plasma membrane; IEP.
GO; GO:0005194; F:cell adhesion molecule activity; IMP.
GO; GO:0007159; P:imaginal disc morphogenesis; IMP.
GO; GO:0007158; P:neuronal cell adhesion; IMP.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR003069; Ig-like.
InterPro; IPR003066; Ig-like.
Pfam; PF00041; fn3; 5.
Pfam; PF00047; ig; 6.
Stapleton M., Brokstein P., Hong L., Agbayani A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 610-814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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Isold=P20241-1; Sequence=Displayed;
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EMBL; AF050084; AAC28613.2; JOINED.
EMBL; AF050085; AAC28614.2; -.
EMBL, AF050084; AAC28614.2; JOINED.
EMBL; AE003444; AAC4837.1; -.
EMBL; AX058284; AAL3513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X76243; CAA53822.1; -.
EMBL; X76244; CAA53823.1; -.
PDB; 1CFB; 30-NOV-94.
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GO; GO:0005886; C:plasma m
GO; GO:0005194; F:cell adh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 4:697-709 (1990).
                                                                                                                                                                                                                                                                                                                        SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
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PRT; 1447 AA

STANDARD;

DCC HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWW----KDGKPLAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 WIKNGKKFDWQAYDNR------MLRQPGRGTLVITIPKDEDRGHYQCFASNEFGTAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 LLLLLIMGGMAQ---DSPPQILVHPQ--DQLF-----QGPGPARMSCRASGQPPFIR 64
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                                                                                                                                                                                                                                                                                          Missing (in isoform Short).
/FTId=VSP 002602.
NR -> KP (IN REF. 2).
MISSING (IN REF. 6).
                                    EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                   CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 6.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
Immunoglobulin domain; Signal; Developmental protein;
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11154
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        Alternative splicing.
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TRANSMEM
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VARSPLIC
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RESULT 15 DCC_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W., Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,
                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Numor suppressor protein DCC precursor (Colorectal cancer suppressor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene DCC in
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-I- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
-I- SUBCELLULAR LOCATION: TYPE I membrane protein.
-I- SUBCELLULAR LOCATION: TYPE I membrane protein.
-I- TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.
-I- DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR POINT MUTATIONS MAY CAUSE BOTH LIMPHATIC AND HEMATOGENOUS METAATASIS OF OBSOPHAGEAL SQUAMOUS CELL CARCINOMAS.
-I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
                                                                                                                                                              Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                             "The DCC gene product in cellular differentiation and colorectal tumorigenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.
WADLINE=94243823; PubMed=8187090;
Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;
Miyake S., and and allelic deletion of tumor suppressor gene Dhuman esophageal squamous cell carcinomas and their relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 4 immunoglobulin-like C2-type domains. SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.
MEDLINE-94245241; PubMed-8188295;
Cho K.R., Oliner J.D., Simons J.M., Hedrick L., Fearon E.R.,
Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;
"The DCC gene: structural analysis and mutations in colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Identification of a chromosome 18q gene that is altered in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 107-472 FROM N.A. (SCRAMBELD EXONS).
MEDLINE=91121517; PubMed=1991322;
Nigro J.M., Cho K.R., Fearon B.R., Kern S.E., Ruppert J.M.,
Oliner J.D., Kinzler K.W., Vogelstein B.;
"Scrambled exons.";
Cell 64:607-613(1991).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
BEDLINE=95011532; PubMed=7926722;
Hedrick L., Cho K.R., Fearon B.R., Wu T.-C., Kinzler K.W.,
Vogelstein B.;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-750 FROM N.A.
MEDLINE=90100559; PubMed=2294591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal cancers.";
Science 247:49-56(1990).
                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                          NCBI_TaxID=9606;
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01-NOV-1995 (
15-SEP-2003 (
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PROMO41; 19; 4

REINTS; PROMO41; 19; 4

REINTS; PROMO61; FN3; 6.

RENART; SMOMO60; FN3; 6.

DR PROSITE; PS6385; IG LIKE; 4.

KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;

KW Repeat; Anti-oncogene; Disease mutation; Polymorphism.

1 25 POTENTIAL.

26 147 EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                  GO: GO: 0004888; F: transmembrane receptor activity; TAS. GO: 0000489; F: axonogenesis; TAS. GO: 00004409; P: axonogenesis; TAS. GO: GO: 00005917; P: induction of apoptosis; TAS. GO: GO: 0007048; P: oncogenesis; TAS. InterPro; IPR003961; FN III.
InterPro; IPR003962; FN III. subd.
InterPro; IPR003962; IQ-11ke.
InterPro; IPR003066; IQ-11ke.
Pfam; PF00041; fn is for interPro; IPR003064; IQ-11ke.
Pfam; PF00041; iq interPro; IPR003064; IQ-11ke.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 3
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                          AAA52175.1; ALT_SEQ.
                                       EMBL; M3229), AAA52176.1;
EMBL; M6366; AAA5217.1;
EMBL; M6370; AAA5217.1;
EMBL; M63702; AAA5218.1;
EMBL; M63718; AAA52180.1;
EMBL; M6368; AAA52181.1;
PIR; A54100; A54100.
HSSP; P56276; ITUK.
Genew; HGNC:2701; DCC.
                    AAA52174.1;
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Matches 68; Conserv
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11;

Gaps

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159 LKCEVIGEPMPTIHWQKNQQDLTPIPGDSRVVVLPSGALQISRLQP------G 205
                                      108 DLGVYTCEASNRLGTAVSR-GARLSVAVLRED-----FQIQPRDMVAVVGEQFTLECG 159
                                                                                                                160 PPWGHPEPTVSWWKDGKPLALQPGRHTVSGGS-ILMARAEKSDEXTYMCVATNSAGHRES 218
                                                                                                                                                                                               219 RAARVSIQEPODYTEPVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXR 275
                                                                                                                                                                                                                          322 SAELTVLVPPWFLNHPSNLYAYESMDIEFECTV-----SGKPVPTV--NWMKNGDVV 371
                                                                                                                                          263 VS-GYPPPSFTWLRGEEVIQLRSKKYSLLGGSNLLISNVTDDDSGMYTCVVTYKNENISA 321
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Search completed: January 30, 2004, 15:55:14 Job time : 11.4663 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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January 30, 2004, 15:51:24 ; Search time 31.9223 Seconds (without alignments) 2449.385 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-047-021-86 1608 1 MGSGGDSLLGGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

. 830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sparches:*
sparches:*
sparches:*
spinus:*
spinus:* SPTREMBL 23:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8wz75 homo sapien	O96jv6 homo sapien	Q8c310 mus musculu	Q8teg1 homo sapien	Q96ms0 homo sapien	O55005 rattus norv	Q9y6n7 homo sapien	O89026 mus musculu	Q90z42 gallus gall	Q8uvd7 xenopus lae	Q90z70 brachydanio	Q9z2i4 mus musculu	Q90z41 gallus gall	Q98sw3 brachydanio	Q90z69 brachydanio	Q9w213 drosophila
SUMMARIES	ID	Q8WZ75	Q96JV6	Q8C310	Q8TEG1	Q96MS0	055005	C976V7	089026	Q90242	Q8UVD7	02060	092214	090241	Q98SW3	692060	Q9W213
	DB	4	4	11	4	4	11	4	11	13	13	13	11	13	13	13	ហ
	T Query Match Length DB	1007	792	1016	702	1034	1651	1651	1612	330	1614	1513	1344	333	1419	1389	1395
•	Query Match	89.8	89.3	69.2	49.2	28.1	27.9	27.8	27.7	27.6	26.9	26.3	25.8	25.3	25.2	25.2	25.2
	Score	1444	1436	1112.5	791	452.5	448.5	446.5	445.5	444.5	432	423	414.5	407	406	405	405
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O44924 drosophila Q9hck4 homo sapien	Q8bj59 aus musculu	Osyppe drosophila Osvpz7 drosophila		O44928 caenorhabdi	09gpp7 drosophila	Q9vq08 drosophila	Q9qzi3 rattus norv	Q90z71 brachydanio	Q92626 homo sapien	Q9qvn5 rattue sp.	Q91z60 rattus norv	P97685 rattus norv	Q96ht1 homo sapien	P97528 rattus norv	O94856 homo sapien	Q961k8 drosophila	Q9vzz4 drosophila	Q9eq17 mus musculu	Q13332 homo sapien	Q8brt6 mus musculu	Q8cbd3 mus musculu	Q8ivul homo sapien	Q64604 r protein-t	Q23991 drosophila	Q8c6x1 mus musculu
5 044924 1 Q9HCK4	11 Q8BJS9	Q9VPZ7	5 001632	6 044928	5 Q9GPP7	800060 9	11 090ZI3	13 Q90Z71	1 092626	11 Q9QVN5	11 091260	11 P97685	1 Q96HT1	11 P97528	094856	5 Q961K8	5 Q9VZZ4	11 09EQ17	1 013332	11 QBBRT6	11 Q8CBD3	1 Q81VU1	11 Q64604	5 Q23991	.1 Q8C6X1
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404.5	398.5	397.5	360	360	358	358	351	348.5	267.5	261.5	261.5	261.5	260.5	260.5	260.5	259	259	258.5	254.5	254	254	253.5	253.5	253	252.5
17	107	7 2 2 2 2 2	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Euteleostomi; Homo.

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Gaps

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Query Match 89.8%; Score 1444; DB 4; Length 1007; Best Local Similarity 98.9%; Pred. No. 2.6e-115; Matches 270; Conservative 1; Mismatches 2; Indels 0;

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181 QPGRHTVSGGSLLIMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
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01-07UN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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                                                                                                                                                                                                                                                                                                                                          PTIRWLINGOPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
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                                                                    A isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
A ranasa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
A ranasa T., Nomura Y., Togiya S., Komai F., Hara R., Takacuchi K.,
A ranasa T., Nabekura T., 1shii S., Kawai Y., Saito K., Takamancto J.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AK02785; BAB5541.1.
R InterPro; IPR001961; FN III.
R InterPro; IPR001906; Ig-MHC.
R Pfam; PF00041; fn3; 2.
R Pfam; PF00047; ig; 2.
R Pfam; PF00047; ig; 2.
R Pfam; PR00066; IG-MHC.
R SWART; SM0060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.3%; Score 1436; DB 4; Length 7 Best Local Similarity 98.5%; Pred. No. 9.5e-115; Matches 269; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 792 AA; 85419 MW; PC6DC05275B7B234 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
11-DRA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14946.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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Q967V6

O1D Q967V6

O1D DT O1-M

DT O1-M

DT O1-M

DD O1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGTAVSRCARLSVAVLREDFOLOPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQ-ALSTDLGVYTCEASNR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 MCSGGTGLIGTEWPLPLLLFIMGGBALDSPPQILVHPQDQLLGGSGPAKMRCRSSGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=22154683; PubWed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
BABL; AKO87355; BAC39850.1; -.
SEQUENCE 1016 AA; 108461 MW; DE70683C63AECDBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLJ00236 protein (Fragment).
FLJ00236.
Momo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
69.2%; Score 1112.5; DB 11; Lengt
Best Local Similarity 77.4%; Pred. No. 7.6e-87;
Matches 212; Conservative 20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to MAGIC ROUNDABOUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RIQLENVTLINPDPAEGPKPRPAVWLXWKVSGP 273
                                                                                                                RIQLENVILLNPDPAEGPKPRPAVWLSWKVSGP 273
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                                                                                                                                                                                                                                                                                  PRT; 1016 AA.
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167

Matches

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41;

Indels

Length 1034;

227

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197 SVSWRXDGARLKEBEGRITIRGGKLMMSHTLKSDAGMYVCVASNWAGERESAAAAEVMVLE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 MSCRASGOPPPTIRWLLNGQPLSMVPPDP--HH-LLPDGTLLLLQPPARGHAHDGQALST 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ISNSSELLIGFNSSLAALNHTILPPGDPSLNGSRVGPEDAMPRIVEQPPDLLVSRGEPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                        1 MGSGGDSLIGGRGSLPLL--LLLIMGGMA------QDSPPQILVHPQDQLFQGPGPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPRDMVAVVGEQFTLECGPPWGHPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Roundabout controls axon crossing of the CNS midline and defines novel subfamily of evolutionarily conserved guidance receptors."; Cell 92:205-215(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98117249; PubMed-9458045;
Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
Goodman C.S., Tear G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 -PQDYTEPVELLAVRIQLENVTLLNPDPAE-----GPKPRPAVWLXWK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 RPSFLRRPV----LRWWLADAPVTFLCEVKGDPPR----LRWR 292
                                                            SMART; SM00060; FN3; 3.
SMART; SM00408; IG22; 5.
PROSITE; PS50835; IG_LIKE; 5.
Hypothetian protein; Immunoglobulin domain.
SEQUENCE 1034 AA; 110723 MW; 09E13C78424F7B30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; S.
Immunoglobulin domain; Receptor.
SEQUENCE 1651 AA; 180747 MW; FA2452DD46E186B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O55005;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                     28.1%; Score 452.5; DB 4;
40.7%; Pred. No. 3.5e-30;
tive 27; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 448.5; DB 1.42.2%; Pred. No. 1.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P56276; ITLK.
InterPro; IRR03961; FN III.
InterPro; IRR00310; Ig-like.
InterPro; IRR003508; Ig_c2.
InterPro; IRR003006; Ig_MHC.
Pfam; PF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF041082; AAC39960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane receptor Robol.
                                                                                                                                                                                                                                                                                                  Best Local Similarity 40.78
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 42.28
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SMART; SM00408; IGC2; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QPGRHTVSGGSLLMARAEKSDEGTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ninomiya K., Wagatsuwa M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Atsuuca T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Atsuuca M., Sato K., Tanikawa M., Ishii S., Yamamoto J., Isono Y., Otsuki T., Sato H., Wakamatu Y., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H., A Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagaiari K., Masuho Y., Nagai K., Isogai T.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

RMBL, AKOS6544; BAB71212.1;
RILEFPO; IPR0019961; FW III.
RILEFPO; IPR001906; FW III.
RILEFPO; IPR003906; Ig-like.
RILEFPO; IPR003006; Ig-MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGSGGDSLLGGRGSLPLLLLLINGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PL/31982.
Hypothetical primates; Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidee; Homo.
                               kuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.; the nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 49.2%; Score 791; DB 4; Length 702; Local Similarity 59.0%; Pred. No. 1.9e-59; nes 161; Conservative 0; Mismatches 2; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGSGGDSLLGGRGSLPLLLLLIM------
                                                                                                                 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074163; BAB84989.1; -
InterPro; IPR0031961; FN III.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR001598; Ig_c2.
InterPro; IPR001306; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D668FEE4BCAFDCC6 CRC64;
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                                                                                                                                                                                                                                                                                                                              Pfam; PP00041; fn3; 2.
Pfam; PP00047; ig; 1.
SMART; SM00060; FN3; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
NOW TER 1
SEQUENCE 702 AA; 75340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75340 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702 AA;
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TISSUE=Spleen;
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Best Local S
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01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2003 (TrEMBLrel. 23,
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                           PRELIMINARY;
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ROBO1 OR DUTTl.
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Q90242;
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                                                                                                                                                                                                    :| ||:|: || || : EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP 123
                                                                           DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
                                                                                                    DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGTLLLLQPPARGHAHDGQALSTDLGVYTÇEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
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Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
Goodman C.S., Tear G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Roundabout controls axon crossing of the CNS midline and defines novel subfamily of evolutionarily conserved guidance receptors."; Cell 92:205-215(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .27.8%; Score 446.5; DB 4; Length 1651;
.larity 41.7%; Pred. No. 2e-29;
Conservative 31; Mismatches 87; Indels 9;
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REMBL; APC040909; ARC39575.1; -.

REMBL; APC040909; RAC39575.1; -.

REMBL; APC040909; RAC39575.1; -.

REMBL; APC040909; ROB01.

RICHEPPO; IPR003106; Ig_MHC.

RICHEPPO; IPR003006; Ig_MHC.

RICHEPPO; IPR003006; Ig_W.

REMBL; SW00041; Ig; S.

REMBL; SW00040; Ig; S.

REMBL; SW000406; IG; S.

REMBL; PS50805; IG_LKE; S.

REQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;
                                                                                                                                                                                                                                                                                                 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Matches 91; Conserva
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MEDINE-21366016; PubMed=11472852;
MEDINE-21366016; PubMed=11472852;
WEYGESSON N., Luria V., Messina I., Erskine L., Laufer E.;
"Expression Patterns of Slit and Robo family members during vertebrate
                                                                                                                                                                                                                                                                                                           Wu M.C., Lowe N., Fordham R., Rabbitts P.; "The mouse homologue of human DUTT1/H-robol gene: protein sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SMART; SMO0406; IGV; 1.
PROSITE; PSO0815; IG 1LKE; 5.
SEQUENCE 1612 AA; 176406 MW; 5F2988C544796B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                    chromosomal location.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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41.7%; Pred. No. 2.4e-29;
tive 31; Mismatches 87;
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01-DEC-2001 (TrEMBLrel, 19, Last seq
01-MAR-2003 (TrEMBLrel, 23, Last ann
                                         Created)
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HSSP; P56276; 1TLK.
MGD; MGI:1274781; Robol.
InterPro; IPR003961; FN III.
InterPro; IPR003106; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-v.
Pfam; PF00041; fn3; 3.
Pfam; PF00047; ig; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                     PPDPHH---LLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDDPRSHRMLLPSGSLPFLR----IVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEV
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connor R.M., Key B.; "Dual role for Roundabout-1 in neural differentiation and axon pathfinding in the Xenopus forebrain."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    27.6%; Score 444.5; DB 13; Length 330;
40.9%; Pred. No. 4.1e-30;
.ive 32; Mismatches 93; Indele 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.9%; Score 432; DB 13; Length 1614; Best Local Similarity 40.6%; Pred. No. 3.5e-28; Matches 89; Conservative 32; Mismatches 88; Indels 10.
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                                                                                                                                                                                                                                    330 330
330 AA; 36725 MW; 0613488F78CEBE61 CRC64;
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Last annotation update)
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               Mech. Dev. 106:175-180(2001).
EMBL; AF364047; AAK94293.1; -
InterPro; IPR007110; 19-1ike.
InterPro; IPR003599; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 3.
PROSITE; PS50835; IG_LKE; 3.
Immunoglobulin domain.
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Immunoglobulin domain.
SEQUENCE 1614
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity 40.99
Matches 94; Conservative
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NCBI_TaxID=8355;
limb development.";
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SEQUENCE
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84

28 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP

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86 SGSLFFIR-----IVHGRKIRPDEGVYVCVARNYLGEAVSHNASLEVAILRDDFRQNPS 139
                                                                                                                               145 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPL-ALQPGRHTVSGGSLLMARAEKSDEX 203
                                                                                                                                                     63 WYKDGERVETDKDDPRSHRMLLPSGSLFLR-----IVHGRRSKPDEGAYVCVARNYLG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 TAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRIKIRGGKLMISNTRKSDAGMYICVGTNMVGERDSETAQVTVPERPTFLRRPTNQVVL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
65 WLLNGQPLSMVPPDPHH---LLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 PGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSI-QEPQDYTEPV----
                                                       85 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 PLLLLLIMGGM-----AQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                        204 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242
                                                                                                                                                                                                                                200 KYVCVGTNMVGERESEVAELTVLERPSFLRRPSNMAVTV 238
                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Roundabout2.
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35.1%; Pred. No. 1.9e-27;
ative 40; Mismatches 97;
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Best Local Similarity
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Query Match
Best Local Similarity 34.5*
Local Similarity 34.5*
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                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMVAVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 SGALFF---PRIVH---GRRSRPDEGVYTCVARNYLGAAASRNASLEVAVLRDDFRQSPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 YMCVASNMAGERESGAAELVVLERPSFLRRPI------NQVVLADAPVNFLCEVQG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ODSPPQILVHPODOLFQGPGPARMSCRASGOPPFTIRWLLNGOPLSMVPPDP--HH-LLP
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROBO2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 25.8%; Score 414.5; DB 11; Length Local Similarity 39.9%; Pred. No. 8.9e-27; es 101; Conservative 27; Mismatches 94; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;
Submitted (PRR.1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF060570; AAD11628.1; -
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Roundabout2 protein (Fragment).
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                        237 EEEAVEFRCOVOG----DPOPS-----IRWK 258
--ELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXWK 269
                                                                                                                                                                                              Created)
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MGD, MGT:1343102; Rbig1.

InterPro; IPR0013961; FullI.

InterPro; IPR003591; Ig. 22.

InterPro; IPR003598; Ig. 22.

InterPro; IPR003006; Ig. MHC.

Pfam; PF00041; fn3; 3.

Pfam; PF00047; ig; 5.

SMART; SM00060; FN3; 3.

SMART; SM000608; IG. 22.

PROSITE; PS50835; IG_LIKE; 5.
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain. SEQUENCE 1344 AA; 1
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                          Rig-1 protein.
RBIG1.
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01-DEC-2001 (
01-DEC-2001 (
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66 LLNGQPLSMVPPDPHH---LLPPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LLLLLIMGGMA-----QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRW
Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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Challa A.K., Beattie C.E., Seeger M.A.;
"Identification and characterization of roundabout orthologs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Imb development."; | Mech. Dev. 106:175-180[2001). | EMBL; ARS40409. | AAK94294.1; - | EMBL; ARS4007110; | EMBL; ARS40094.1; - | EMBL; ARS
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Transmenbrane receptor Roundabout3.
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MEDLINE=21366016; PubMed=11472852;
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EMBL, AF904131; AAK28043.1; -.
HSSP, P08921; 1A64.
ZFIN; ZDB-GENE-000209-4; robo3.
INCEPPO; IPR003962; FNII subd.
InterPro; IPR003961; FNIII.
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MEDLINE=21270059; PubMed=11376489;

Lee J.S., Ray R., Chien C.B.;

Lee J.S., Ray R., Chien C.B.;

Lee J.S., Ray R., Chien C.B.;

T coles in axon guidance and cell migration.";

Lov. Dyn. 221:215-215-230(2001).

EMBL; AF837036; AAK56428.1; -...

R ZFIN; ZDB-GENE-000209-4; robo3.

R InterPro; IPR001956; FMIII subd.

InterPro; IPR001956; FMIII.

InterPro; IPR001961; FW III.

InterPro; IPR001598; Ig-C2.

R InterPro; IPR001506; Ig-HkC.

R Pfam; PF00041; En3; 3.

R Pfam; PF00041; Ig.; 5.
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                                                                                                                                                                                             Query Match 25.2%; Score 406; DB 13; Length 1419;
Best Local Similarity 36.1%; Pred. No. 5.1e-26;
Matches 97; Conservative 36; Mismatches 100; Indels 36; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
Cyprinidae; Danio.
             InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00041; fi3; 3.
Pfam; PF00041; fi3; 3.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00066; FN3; 3.
SWART; SM00408; IGc2; 5.
PROSITE; PSSO835; IG_LIKE; 5.
Immunoglobulin domain; Receptor; Repeat.
SEQUENCE 1419 AA; 155381 MW; DIB3C0940D6CCEFE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SMART; SM00060; FN3; 3.
SMART; SM0408; IGC2; 5.
FNSYTE; PS50835; IG_LIKE; 5.
Immunoglobulin domain; Repeat.
SEQUENCE 1389 AA; 151913 MW;
 InterPro; IPR007110; Ig-like.
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January 31, 2004, 12:28:30 ; Search time 1838.41 Seconds (without alignments) 4005.776 Million cell updates/sec
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1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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ALIGNMENTS

BC039602 3758 bp mRNA linear HTC 06-NOV-2002 Homo sapiens, Similar to roundabout homolog 4, magic roundabout (Drosophila), clone IMAGE:5590503, mRNA. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3758) BC039602 BC039602.1 GI:24660430 Homo sapiens (human) RESULT 1 BC039602 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION REFERENCE

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180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cS0D1075CH07QPl&cluster=6206.r. Contact :
Feng Liang Email: fliang@lifetech.com WR. :
Feng Liang Email: fliang@lifetech.com WR. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope Sequence ID : CS0D1075CH07QPl.
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/db_xref="taxon:9606"
/clone="CSDD1075YP13"
/tissuc type="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu
                                                                                                                                                                                                                                            GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer
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                                                                                                               449 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTCTGGAATGTGGGCCG
                                                                                                                                                                                                                                                                                      AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal
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                        Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-25590,
                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: i COlumn: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessies Eshey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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clone_lib="NIH_MGC_125"
                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
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Matches:
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Mismatches:
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1232 c 1046 g 708 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590503"
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                                                                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. 381 c 369 g 212 t 36 others
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Best Local Similarity:
Query Match:
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mRNA linear EST 12-MAR-2002 sapiens cDNA clone IMAGE:5753515
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12789 row: g column: 20
High quality sequence stop: 697.
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Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo
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Homo sapiens
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/tissue type="FETAL BRAIN"
/dev stage="fetal"
/dev stage="fetal"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

286 c 177 g 158 t 12 others
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 /clone="CS0DF001YI24"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqrefégenoscope.ns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODF001BB12QP1&cluster=6206.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: fliang@lifetech.com URL :
Location/Qualifiers

Location/Qualifiers
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BX418142 BX418142.1 GI:30642200
                GluAlaSerAenArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
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1 (bases 1 to 922)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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In (Dates 1 to 2004).

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM361 row: 1 column: 16

High quality sequence stop: 578.
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                                                                                               HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AlaArgValSerIleGlnGlu-ProGlnAspTyrThr-GluProVal-GluLeuLeu--- 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758 TGTGCGAATTTCAGCTGGGAAAATGTGACACTGGCTGGAACCCCGGATCCTGGCAAAGGG 817
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Ammanlia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis
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Email: cgapbs remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: c column: 24
High quality sequence stop: 637.
Location/Qualifiers
                                                            CB994099

AGENCOURT 13642710 NIH MGC 148 Homo sapiens cDNA clone
MAGE:30331943 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="dorsal root ganglia"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab host="BH10B"
/clone | Lib="Lupski dorsal root ganglion"
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/clone | Lupski dorsal root ganglion"
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Not1; Site_2: Sall; cDNA made by oligo-dT priming:
Directionally cloned using the following adaptors:
Directionally cloned using the following adaptors:
S'-TCGACCAGGCTCG-3' and
S'-TCGACCAGGCTCG-3' and
S'-TCGACCAGGCTCG-3' and
S'-TCGACCAGGCTG-3' Site selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
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AGENCOURT 7982449 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6186214 5', mRNA sequence.
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
Location/Qualifiers
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                                                221 AlaArg-ValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVa
GACGAAGGGACCTACATGTGTGTGCCACCAACAGCGCAGGACATAGGGAAGAGCCGCGCA
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                                                                                                         698 GCCCGGGGTTTCCATCCAGGAA---
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AK004723 3689 bp mRNA linear HTC 05-DEC-2002 Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012D01 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

AK004723 LOCUS DEFINITION

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Gojobori, T., Bono, H., Kandkawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Relischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Fesole, G., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Bofielli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshhaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (202)

6 (bases 1 to 3689)
                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
AK004723.2 GI:26334429
HTC; CAP trapper.
Mus musculus (house mouse)
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TITLE JOURNAL

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MATURAQERSRAARVSI GESQDHKEHLELLAKT ROLENVILLANBEPVRGFREGPSVW
LSWKVSGPALPARGSYTAL FRYTGSFRDQSFWTFULIAGLQSAKLGGIHWGOPYEFKV
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EQAMEQSARDPRKHYWTLEQLRATIRRPEVIASSSVCVQVAANTGAGAGELSTPVCLILL
EQAMEQSARDPRKHYWTLEQLRATIRRPEVIASSSVCVQVAANTGAGAGELSTPVCLILL
RQAKEQSARDPKHYPWTLEQLRATIRRPEVIASSSVCVQVAANTGAGAGELSTPVCLILL
RQAKEGSARDFKHYRMDHSDSPWIADTWRSTSGGRDLSSSSSLSSRLGLDPRDP
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/translation="MGGEEPRAPMGSGGTGLLGTEWPLPLLLLFIMGGEALDSPPQI
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PSVQGRPQDDQNILSAILGVYTCEASNRLGTAVSRGARLSVAVLQEDFQIQPRDTVAV
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TSSPWASSDSLCSRRGLCSPRMSLTPTEAWKAKKKQELHQANSSPLLRGSHPMEIWAW
ELGSRASKNLSQSPGEAPRAVVSWRAVGPQLHRNSSELASRPLPPTPLSLRGASSHDP
                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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AGGGVGSEVGNLLYPPRPCPTPTPSEGSLANGWGSASEDNVPSARASLVSSSDGSFLA
DTHFARALAVAVDSFGLSLDPREADCVFTDASSPPSPRGDLSLTRSFSLPLWEWRPDW
                                                                                                                                                                                                                                                                                                                                                                                                                   On Dec 10, 2002 this sequence version replaced gi:12836108. Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
     Shiraki, T., Sogabe, Y.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,N Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
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/strain="C57BL/6J"
/db_xref="FANTOM D8:1200012D01"
/db_xref="MG1:1907253"
/db_xref="taxon:10090"
/clone="1200012D01"
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/organism="Mus musculus"
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HTC 05-DEC-2002

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3865 bp

AK087355

BASE COUNT ORIGIN

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/clone_lib="RKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
1. .3054
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,Y., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Saeaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Direct Submission
                                                                                                                                                                                                                                                                                              Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama (Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, NRL:http://genome.gsc.riken.go.jp, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Bncyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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similar to MAGIC ROUNDABOUT [Homo sapiens] (SPTR|AJ
evidence: FASTY, 77.6%ID, 99.5%length, match=3012)'
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
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/db_xref="GI:26352440"
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       Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030049917 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 3865)
                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                        GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro
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803 bp mRNA linear EST 01-MAY-2003 C_148 Homo sapiens cDNA clone

AGENCOURT 13623935 NIH MGC 148 Ho IMAGE:30336795 5', mRNA sequence.

CB997292

DEFINITION

LOCUS

CB997292.1 GI:30291812 EST. Homo sapiens (human) Homo sapiens

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 8013)
NIH-MGC http://mgc.noi.nih.gov/.
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                                                                                                   Email: cgapbs-remail.inh.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with he
and advice from Piero Carnino! (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM360 row: n column: 04
High quality sequence stop: 535.
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Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30336795"
                                                                                          Contact: Robert Strausberg, Ph.D.
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Length: Matches: Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMI141 row: g column: 21
High quality sequence stop: 723.
Location/Qualifiers
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1 (bases 1 to 729)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
|SerArgGlyAlaArgLeuSerValAlaValLeuArgGluAgpPheGln
                                                                                                                                                              398 GCCACGCAGTCAGCAGAGGCGCTCGCGTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG
                                                                         | IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro
                                                                                                     458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGAGCAGTTTACTCTGGAATGTGGGCCC
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Homo sapiens
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1230 bp mRNA linear EST 12-MAR-2002
_6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503
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Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: NDAM381 row: 1 column: 13
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1 (bases 1 to 771)
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14 "Mac http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                  CCCTGGGGCCACCCAGAGCCCACACTCCATGGTGGAAAGATGGAAAACCCCTGGCCCTC
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/lab_host="DH10B"
/clone="Drgan: ovary" (pool 6 3); Vector: pCMV-SPORT6;
/note="Organ: ovary" (pool) Site 2: Not!; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

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1 (bases 1 to 1230)
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12364 row: o column: 16
High quality sequence stop: 535.
Location/Qualifiers
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Homo sapiens cDNA clone co. c.
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Email: cgapbs-r@mail.uth.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: THe I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://mage.llnl.gov
Plate: NDAM390 row: a column: 12
||| :::::: ||| ::::| ||| 666 AGAGGGACCANNCCAACAGGGGAAGGAAC 725
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Mcioael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDAM392 row: p column: 08
High quality sequence stop: 448.
      CTCATCATGGGAGGCATGGCTCAGGACTCCCGGCCCCAGATCCTAGTCCACCCCCCAGGAC 157
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 688)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Search completed: January 31, 2004, 15:28:18 Job time : 1848.41 secs

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January 30, 2004, 15:44:59 ; Search time 35.7513 Seconds (without alignments) 1225.369 Million cell updates/sec
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GenCore version (c) 1993 - 2004
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number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution. Pred. No. is the number of res score greater than or equal to and is derived by analysis of

		Description	Human secreted pro	Amino acid sequenc	Human TANGO 330 fo	Human PRO860 prote	Human PRO860 (UNQ4	Human PRO860 polyp	Novel human protei	Human ECSM4 protei	Human protein sequ
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ALIGNMENTS

ABP62033 standard; Protein; 303 AA.

RESULT 1 ABP62033

(first entry)

12-NOV-2002

ABP62033;

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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthitic; cancer; antirheumatic; hepatotropic; cerebroprotective; antinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
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R, Brewer LA;
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"secreted protein"

28..303 /note= "

/note= "signal peptide"

Location/Qualifiers

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New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders, tumours, immune disorders, inflammation or haematological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 190-191; 215pp; English.
                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-204988/17
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                                                                                                                                                                                                                                                                                                                                   Rosen GA,
              Key
Peptide
                                                     Protein
The invention relates to novel genes (AB092553-AB092607) and proteins (ABD62013.4BP62153) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast on ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune throughtie, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial schaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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                                                 New polynucleotides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                      99.6%; Score 1469; DB 23;
100.0%; Pred. No. 1.5e-121;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKVSGPXRLPNLTRPCSGPRLPREARELRGQRRNTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 1; 785pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.6
Best Local Similarity 100.
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                               parasitic infections.
           2002-599716/64.
                                                                                                                                                                                                                                                                                                                                                                            303 AA;
                          N-PSDB; ABQ92573
                                                                                              disorders
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Lafleur DW, Moore PA, Olsen HS; Shi Y;

Ebner R, Ruben SM,

97US-0057669. 97US-0058666. 97US-0058667. 97US-0058973.

97US-0057626 97US-0057663 97US-0058974

98WO-US18360

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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVVGEQPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
AAY12914-68 represent human secreted proteins. The polypeptides and their corresponding polynucleotides are useful for preventing. treating or ameliorating medical conditions, e.g. by protein or gene treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the presence of mutations in the new polyneptides in a sample or by determining the presence of mutations in the new polynectides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, allergy, hematopoietic disorders, astehma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
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0
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100.0%; Pred. No. 1.5e-121;
iive 0; Mismatches 0;
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Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 304 AA;
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Human secreted protein; cancer; immune disorder; infection; inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disorder; arthritic disorder; asthma; immunodeficiency disease; AIDS;

transplant rejection; ss.

Homo sapiens

Amino acid sequence of a human secreted peptide.

(first entry)

17-JUN-1999

AAY12934;

AAY12934 standard; Protein; 304 AA

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Modified-site
                                                                                                                 05-APR-2001
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                                                                                                                       Human; TANGO 315; clone JthxelBlel2; TANGO 330; TANGO 437; TANGO 480;
cellular process regulator; gene therapy; astrocyte; cancer;
Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
cell proliferative disorder; neurological disorder; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Protein kinase C phosphorylation site" 386..388 /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                           /note= "cAMP and cGMP dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98..300
note= "Protein kinase C phosphorylation site"
125..330
                                                                                                                                                                                                           "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                 note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                               "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                    note= "Protein kinase C phosphorylation site"
52..157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                  WKVSGPXRLPNLTRPCSGPRLPREARELRGQRRNTG 276
                 268 WKVSGPXRLPNLTRPCSGPRLPREARELRGGRRNTG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..280
.te= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                              "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                              "N-myristylation site"
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                                                                                                                                                                                                                  21..480
/label= Extracellular_domain
                                                                                                                                                                                                                                                                   phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                             "N-myristylation
                                                                                                                                                                                                                                                                                       77.147
/label= Ig-like_domain
                                                                                                                                                                                      1..20
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                        'label= Ig-like_domain
                                                                                                                                                                             Location/Qualifiers
                                                            AAU00501 standard; Protein; 480 AA
                                                                                                        Human TANGO 330 form 2 protein.
                                                                                          (first entry)
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133..138
                                                                                                                                                                                                                                                                                                                                                                                                                                                ..239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..258
                                                                                                                                                                                                                                                                                                                       100..105
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/note=
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                                                                                          18-JUL-2001
       241
                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                    Domain
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The present sequence representing human TAMGO 310 form 2 is isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA library. TAMGO 310 is 1 of 4 movel human transmembrane proteins.

CC library. TAMGO 310 is 1 of 4 movel human transmembrane proteins.

CW which also includes TAMGO 315 (AAU00498-AAU00499), TAMGO 437 (AAU00502)

CM and TAMGO 480 (AAU00503). The nucleic acids encoding these proteins

CC are useful as modulating agents in regulating a variety of cellular

CC processes and can be used to express the proteins in a host cell in

CC pene therapy applications. Antisense nucleic acid molecules and

CC expression vectors containing the TAMGO nucleic acids are also described.

CC Diagnostic assays can be used to detect genetic alterations in the TAMGO

CD contein and to identify, compounds that bind to or modulate activity

CC of the TAMGO proteins. Anti-TAWGO antibodies are used diagnostically to

CM conticor protein levels in tissue as a clinical testing procedure.

CM and proteins may be used to diagnose, treat and monitor disorders of the

CA and proteins may be used to diagnose, treat and monitor disorders of the

CA and proteins may be used to treat call prolliferative disorders (e.g. cancer),

CM and neurological disorders e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
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456..461
/note= "N-myristylation site"
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Pred. No. 2.4e-107,
1, Mismatches 2,
                                                                                             420..423
/note= "Asn is N-glycosylated"
                                                                                                                                                           427..430
/note= "Asn is N-glycosylated"
"Asn is N-glycosylated"
                    ...413
ote= "N-myristylation site"
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98.8%;
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Matches 243; Conservative
                                                                                                                                                                                                                         435..438
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Query Match
239 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLS 298
                                                                                         Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                                               AAY41716 standard; Protein; 985 AA
                                                                               Human PRO860 protein seguence.
                                                                                                                                                                                                  98US-0078910.
98US-0078936.
98US-0078939.
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980S-0079689.
980S-0079728.
980S-0079786.
980S-0079923.
980S-0080105.
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98US-0077641.
98US-0077649.
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98US-0078004.
98US-0040220.
98US-0078886.
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98US-0080194.
98US-0080327.
98US-0080333.
98US-0080334.
98US-0081.049.
98US-0081.049.
98US-0081.070.
98US-0081.070.
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98US-0082804.
98US-0082767.
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98US-0081817
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98US-0079
          241 WKVSGP 246
                    299 WKVSGP 304
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22-APR-1998;
23-APR-1998;
                                                                                                               Homo sapiens
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31-MAR-1998
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 77; 530pp; English.
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98US-0084640.
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98US-0085339.
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98US-0083322
98US-0083329
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N-PSDB; AAZ34069.
                                                                               29-APR-1998
29-APR-1998
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88.9%; Score 1311; DB 20; Length 985;

985 AA;

invention. Sequence

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16-OCT-2001; 2001US-0978697.
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                                   cellular activities
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 N-PSDB; AAC78502.
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                         1. QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRWLLNGQPLSMVPPDPHHLLPDGT
                                   6 QDSPPQILVHPQDQLFQGPGRAKSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLPDGT
                                                                                            121 AVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALOPGRHTVSGGSLLMARAEKSDEXTYMC
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         Gaps
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Fong S, Gao W, Gerber H, Gerritsen ME;
Grimaldi CJ, Gurney AL, Hillan KJ;
ier MA, Pan J, Paoni NF, Roy MA;
Tumas D, Williams PM, Wood WI;
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        Indela
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98.8%; Pred. No. 5.7e-107;
        1; Mismatches
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TA, Tumas D,
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99WO-US31243,
99WO-US31274,
2000WO-US0219.
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99US-0126773.
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99US-0134287.
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99WO-US28565
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06-JAN-2000; 2000WO-US00376
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Filvaroff E,
Godowski PJ,
Kuo SS, Nap
        243; Conservative
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Similarity
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                                                                                                                                                                                                                                   AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to Kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate
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Pred. No. 5.7e-107;
1; Mismatches 2;
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3est Local Similarity 98.8%;
Aatches 243; Conservative 1
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98US-077641P.
98US-077641P.
98US-07791P.
98US-078004P.
98US-078910P.
98US-078936P.
98US-078936P.
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99WO-US12252
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99US-0311832
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12-APR-1999;
14-MAY-1999;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bloactive molecules to cells expressing PRO polypeptides, for linking bloactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The bloactive molecule maybe a toxin, radiolabel or antibody, and causes apprepriate molecule maybe a toxin, radiolabel or antibody, and causes bloactive molecule maybe a toxin, radiolabel or antibody, and causes apportive molecule maybe a toxin, radiolabel or antibody, and causes apportive molecule maybe a toxin, radiolabel or antibody, and causes apportive molecule maybe at toxin, radiolabel or antibody, and causes are adiac insufficiency, nervous system disorders, kidney disorders, cardiac insufficiency, nervous system disorders, and wound healing. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for analysis of individuals with genetic disorders, and in gene therapy.
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Ferrara N, Filvaróff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent, was obtained in electronic format directly from the USPTO web site.at seqdata.uspto.gov/psipsDIDEntry.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
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                                                                                               2000US-0747259.
2001US-0816744.
2001US-0816920.
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2001US-0854280.
2001US-0872035.
2001US-0874503.
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19-JUN-2001; 2001US-0886342.
30-JUL-2001; 2001US-0918585.
                99US-0380138.
99US-0380142.
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Matches 243; Conservative
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N-PSDB; ABX92441.
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                25-AUG-1999;
25-AUG-1999;
08-NOV-2000;
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22-MAR-2001;
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121 AVVGEQPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC
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                                   186 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLINPDPAEGPKPRPAVWLS 245
               VATINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopolesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                  Human, antianaemic, vulnerary, antiinflammatory, immunomodulator,
antiinfertility, cerebroprotective, cytostatic, rheumatic, gene therapy,
neuroprotective, antiparkinsonian, protein therapy, EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1311; DB 23;
Pred. No. 5.8e-107;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang J,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 578; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asundi V, 2
F, Drmanac F
                                                                                                                                                                                     ABB97310 standard, Protein; 1007 AA.
                                                                                                                                                                                                                                                                                    Novel human protein SEQ ID NO: 578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Zhou P, Asu
Yang Y, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2001; 2001WO-US26015.
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                                                                                                                                                                                                                                                     (first entry)
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Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-292408/33.
                                                                         241 WKVSGP 246
                                                                                                       246 WKVSGP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN32496.
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200222660-A2.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                     27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
Xue AJ,
               181
                                                                                                                                                                                                                     ABB97310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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207
                                                    VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                         208. VAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynuclectide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopachy, neovasculatures or memorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation, detecting a tumour or tumour neovasculature, cardiac disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endometriosis; hypoxic condition; angiogenesis; cytostatic; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                 AAU99419 standard; Protein; 1104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 53; Fig 12; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents human ECSM4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001; 2001WO-GB04906
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                                                                                                                                                                                                                                                                                                                                              07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-508120/54.
                                                                                                                             WKVSGP 246
                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                                                                     Human ECSM4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK87137.
                                                                                                                                                                    WKVSGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                          AAU99419;
              148
                                                    181
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1104 AA;

Sequence

88 LILLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFOLOPRDMV 147

61 LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120

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Gaps

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Indels

9 87

1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT 28 QDSPPQILVHPQDQLFGGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT

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                                                                                                   LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPRDMV 120
                                                                                                                  88 LILLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 147
                                                                                                                                                 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                                                                                                                                                                 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMC 207
                                                                                                                                                                                             VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                    208 VATNSAGHRESRAARVSIQEPODYTEPVELLAVRIQLENVTLINPDPAEGPKPRPAVWLS 267
                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNBA defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                    28 QDSPPQILVHPQDQLFQGPGPARMSCQASGOPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                        ODS PPO1LVHPODOLFOGPGPARMSCRASGOPPPT1RWLLNGOPLSMVPPDPHHLLPDGT
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   detection; diagnosis; antisense therapy; gene therapy
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            Length 1104;
                                 Indels
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         Score 1311; DB 23;
Pred. No. 6.5e-107;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; SEQ ID 18085; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:18085
                                                                                                                                                                                                                                                                                                                            AAB95515 standard; Protein; 792 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
          88.9%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0248036
                     Best Local Similarity 98.8
Matches 243; Conservative
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                                                                                                                                                                                                                                           WKVSGP 246
                                                                                                                                                                                                                                                                 268 WKVSGP 273
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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            Query Match
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LILLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence; at least 15 nucleotides and the combination of the 5'-end sequence; at least 15 nucleotides and the combination of the specification. The primers sets can be used in antisense therapy and particularly full-length cDNAs. The primers are also useful for the principal particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AAH13632 represent human coll sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent coligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ODSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human protein kinase/protein phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, protein kinase, protein phosphatase, signal transduction,
intracellular signalling pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1303; DB 22;
Pred. No. 2.2e-106;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               88.3%;
ilarity 98.4%;
Conservative 1
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18-JOAN-2000; 2000JP-0118776.
11-JAN-2000; 2000JP-0118776.
17-FEB-2000; 2000JS-0183322.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                 the present invention
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tes 242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               792 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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(IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  06-NOV-2000; 2000US-245566P.
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                                                                                                                                                                                                                                                                                                                                                                                  88 LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 147
                                                                                                                                                                                                                                                                                                                                                                                                         AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLINPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 VAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNDDPAEGPKPRPAVWLS 267
                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                   The present sequence represents a human protein kinase/protein phosphatase. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used
                                                                 New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                     148 AVVGEQPTLECGPPWGHPEPTVSWWKDEKPLALQPGRHTVSGGSLLMARAEKSDEGTYMC
                                                                                                                                                                                                                                                                                                                          28 QDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLDFDGT
                                                                                                                                                                                                                                                                                                              QDSPPQILVHPQDQLPQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                                         Gaps
  Funahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease;
                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                  Length 792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endometriosis; hypoxic condition; angiogenesis; cytostatic
cardiant.
  Otsuki T,
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                Score 1303; DB 22;
Pred. No. 2.2e-106;
  Nagai K,
                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                     target molecules fir drug development
                                                                                                               Claim 2; Page 175-180; 336pp; Japanese.
  Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU99420 standard; Protein; 1015 AA
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.4%;
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001; 2001WO-GB04906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ECSM4 protein #1.
 Sugiyama T,
                                  WPI; 2001-564736/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 WKVSGP 273
                                                                                                                                                                                                                                          792 AA;
           Nezu J;
                                             N-PSDB; AAH78073
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Ishii S,
Senoo C,
                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                          61
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The present invention relates to endothelial cell-specific molecule 4 (BCSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnosit or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac consistence, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogeness in an individual. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLQPPARGHAHDGQ-ALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPRDMV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLHRPSVQGRPQDDQNILSAILGVYTCEASNRLGTAVSRGARLSVAVLQEDFQIQPRDTV
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                                                                                                                                                                                         Novel endothelial cell-specific molecule polypeptide 1 or 4, usefu imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
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                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 13; 248pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00500 standard; Protein; 934 AA
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Bicknell R, Huminiecki L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 78.5
Matches 193; Conservative
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                                                                                                                 N-PSDB; ABK87138
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'note= "Protein kinase C phosphorylation site"
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532..635
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N-PSDB; AAS01694.
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                                                                                                                                                                                                                                                                                                                      Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia; cell proliferative disorder; neurological disorder; Alzheimer's disease
                                                                                                           /note= "Alternatively this residue is Asp due to species variation"
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                                                                                                                                                                        3
/note= "Alternatively this residue is Val due to
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species variation"
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/note= "Casein kinase II phosphorylation site"
455..457
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/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                         .154
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..196
te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..284
te= "Protein kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91..393
note= "Protein kinase C phosphorylation site"
                                                                                                                                   2
/note= "Alternatively this residue is Ser due
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                                                                                                                                                                                                                                                                                                                                                                                                        "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..176
te= "Asn is N-glycosylated"
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note= "Asn is N-glycosylated"
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:e= "Asn is N-glycosylated"
                                                                                                                                                                                                                       "N-myristylation site"
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                                                                          1..393
/label= Extracellular_domain
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                                                                                                                                                                                               species variation"
                                                                                                                                                           species variation"
                                                                                                                                                                                                                                                                                                                                                                                label= Ig-like_domain
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .319
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'note=
                                                                                                Misc-difference
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                                      Homo sapiens
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Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
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/note= "Protein kinase C phosphorylation site"
929..932
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                    .561
e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                              11..714
note= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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194..797
/note= "Casein Kinase II phosphorylation site"
                                                                                                        53..555
note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                             "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                            21..724
note= "Casein kinase II phosphorylation site"
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note= "Protein kinase C phosphorylation site"
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"Protein kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .735
.e= "Casein kinase II phosphorylation
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te= "Asn is N-glycosylated"
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domain

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DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of a novel human protein designated T85, and also referred to as FMHB-6D4 and FMHB-SD4. T85 cDNA (see AAV66278) was identified in a human foetal brain cDNA library using secreen designed to identify genes encoding protein having a functional signal sequence. T85 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying a variety of cellular to modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological
  "has homology to a Ig superfamily domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 753;
                                                                                                                                                                                                   /note= "cytokine receptor homology N-terminal
                                       "has homology to a Ig superfamily
                                                                                                                    to a 1g superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Indels
                                                                               "has homology to a Ig superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 YVCVGTNMVGERESEVAELTVLERPSFVKRPSNLAVTV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.3%; Score 446.5; DB 2
41.7%; Pred. No. 9.2e-31;
iive 31; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                         ...491
---= "has homology
                                                                                                                                                            'note= "RGD motif"
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                                                                                                                                                                                                                        domain"
                                                                                                                                                                                                                                                                                                                                           98WO-US07714
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              /note= "h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holtzman D, McCarthy SA;
                                                          .394
                                                                                                                                         247..249
                                                                                                                                                                               516..600
  /note=
                                                                                   note=
                                                                                                                        note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               753 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV69278
                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1997;
                                                                                                                                                                                                                                                                WO9848051-A2
                                                                                                                                                                                                                                                                                                                                           17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-1997;
                                                                                                                                                                                                                                                                                                     29-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                       Peptide
                                                            Region
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                                                                                                                                                                                 Domain
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                             The present sequence representing human TANGO 330 form 1 is isolated from cDNA clone jthAa060g22 from a human adrenal gland cDNA clone jthAa060g22 from a human adrenal gland cDNA library. TANGO 330 is 10 f 4 novel human transmembrane proceins which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins care useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acid molecules and carpostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity compounds to protein levels in tissue as a clinical testing procedure. TANGO proteins Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids and proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat cell proliferative disorders (e.g. cancer), and neurological disorders e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 QFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCVATNS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 QFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMCVATNS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 PPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFOLOPRDMVAVVGE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 PPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFOLOPRDMVAVVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/note= "has homology to a 1g superfamily domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T85; FHMB-6D4; FMHV-SD4; human; neurological disorder; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "has homology to a fibronectin type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "has homology to a fibronectin type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 955; DB 22;
Pred. No. 1.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21..753
/label=_Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
Claim 9; Fig 13; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW83927 standard; Protein; 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.9
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145..203
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                                                                                                                                                                                                                                                                                                                                                                                                                          934 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis.
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                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.

The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified pulpeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MRC-binding polypeptide. The polypeptides and polymoclecides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, clymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expenses depotein tag (EPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
                                                                                                                                                                                                                                           Translational profiling, expressed protein tag; EPT; kinase, phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer;
                                                                                                                                                                                                                                                                                                                                              gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obtained in electronic format directly fr
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID No 756; 134pp; English
                                                                                                                                                                                                Human expressed protein tag (EPT) #756
                                                ABU04090 standard; Protein; 753 AA.
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2001US-310801P.
2001US-326370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002WO-US09671.
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2002US-358985P.
                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-040607/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYCO-) ZYCOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200278524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2001;
20-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001;
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                                                                                                                                                29-JAN-2003
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                                                                                                ABU04090;
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RESULT 14
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ABU0

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ABU0

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ABU0

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ABU0

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This invention describes novel Robo (roundabout) polypeptides, involved in nerve guidance which heve been isolated from Drosophila sp., C. elegans, human and murine samples. The products of the invention can be used to raise anti-Robo antibodies, which can be used to modulate cell function or morphology. The Robo polymucleotides and fragments are useful as probes and primers and for production of the Robo polypeptides. The probes and primers are also useful in screening assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                       123
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                                                                                                          DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 117
                                                                                DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roundabout; nerve guidance; human; murine; cell function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR
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41.7%; Pred. No. 2.4e-30;
tive 31; Mismatches 87; Indels 9;
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                                                                                                                                                                                               178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             morphology; screening assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidd T,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-312615/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ROBOl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1649 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX08404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROBO2;
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TYPE: PRT
ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 Application US/09540245A

Patent No. 6270984

GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Rid, Thomas
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFREENCE: B98.031-3
CURRENT APPLICATION NUMBER: US/09/540,245A

PRIOR APPLICATION NUMBER: 60/065,544
PRIOR PILLING DATE: 1997-11-14
PRIOR PILLING DATE: 1997-11-14

PRIOR FILING DATE: 1997-11-14

PRIOR FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN NOS: 20
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US-09-638-649-1

US-09-707-802-10

US-09-707-802-10

US-09-707-802-10

US-09-130-1386-14

US-09-130-1386-14

US-08-152-307B-7

US-09-991-326-7

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                                                                                                                                                                                                                                                                                                                                                                                                 Length 1395;
                                              APPLICANT: Bross, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B99-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/061,057
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1395
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APPLICANT: Erose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: (05/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.8%; Score 395.5; DB 3; Length Best Local Similarity 37.1%; Pred. No. 8.1e-31; Matches 92; Conservative 35; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09540245A Patent No. 6270984 GENERAL INFORMATION: APPLICANT: Goodman, Corey APPLICANT: Kid, Thomas
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; ORGANISM: Drosophila melanogaster
US-09-540-245A-15
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APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Karja
APPLICANT: Brose, Karja
APPLICANT: Tessder-Lavigne, Marc
ITILE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR PILING DATE: 1999-11-14
PRIOR PILING DATE: 1999-11-14
SHOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTIN Ver. 2.0
44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 PKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|: : | | :| | :| PQPQ----ITWK-----RKNEPMPVTRAYIAKDNRGLRIER 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLPDV--LWR------RTASGGNMP 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09540245A Patent No. 6270984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.7%;
Matches 91; Conservative
   96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-540-245A-16
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Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                         Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PQILVHPQDQLPQGPG-PARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 ------RDTQIGSS--AVYQCNASNEHGYLL---ANAFVSVL----DVPPRILAPRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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17.0%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels
                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-No. 6191586-2000
CLASSIFICATION: <a href="https://doi.org/10.10m/">CLASSIFICATION: <a href="https://doi.org/">cUnknown</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PAPPLICATION UNDBER: 08/752,307
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 GIYTCVATNILGKVEAQ-VRLEVKDP 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 XTYMCVATNSAGHRESRAARVSIQEP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09991326
Patent No. 6395872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 630 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McCarthy, Sean A. Gearing, David P.
Gearing, David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 14
                                                                                             NUMBER OF SEQUENCES: 14
                                                                                                                                                                                      CITY: Boston
STATE: MA
                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-707-802-14
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                                        Sequence 14, Application US/08752307B
Patent No. 5952171
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 ------RDTQIGSS--AVYQCNASNEHGYLL---ANAFVSVL----DVPPRILAPRN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 QLIKVIQYNRTRLDC-PFFGSPIPTLRWFKNGQGNMLDGGNYKAHENGSLEMSMARKEDQ 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Indels
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESQ for Windows95
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/752,307B
FILING DATE: 19-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: SPRING APPLICATION NUMBER: APPLICATION NUMBER: ATTORNEY AGENT INFORMATION:
NAME: Malklejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Score 251; DB 2;
34.5%; Pred. No. 8.9e-17;
tive 34; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09404/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 XTYMCVATNSAGHRESRAARVSIQEP 201
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09707802
Patent No. 6391586
GENERAL INFORMATION:
APPLICANT: MCCArthy, Sean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
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617-542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                         US-08-752-307B-14
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                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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APPLICANT: MCCarthy, Sean A.
APPLICANT: MCCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 LVIMNP-----TKAQDAGVYQCLASNPVGTVVSREAIILRFGFLQE-FSKEERDPV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 -AVVGEOFTLECGPPWGHPEPTVSWWKDGKPLAL-OPGRHTVS--GGSLLMARAEKSDEX 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 KAHEGWGVMLPCNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTTGNLYIARTNASDLG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 TYMCVAINSAGHRE----SRAARVSIQ------EPQDYTEPVELLAVRIQLE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 NYSCLATS---HMDFSTKSVFSKFAQLNLAAEDTRLFAPSIKARFPAETYALVGQQVTLE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.5%; Score 228; DB 2; Length 607; 29.5%; Pred. No. 1.7e-14;
                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,307B
FILING DATE: 19-NOV-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.5%; Score 228; DB Best Local Similarity 29.5%; Pred. No. 1.7e-Matches 79; Conservative 38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
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ADDRESSEE: Fish & Richardso:
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09707802
Patent No. 6391586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
REGISTRATION NUMBER: 35,2
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ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 607 amino acids
amino acid
                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                      COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-752-307B-12
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Patent No. 5952171
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 ------RDTQIGSS--AVYQCNASNEHGYLL---ANAFVSVL----DVPPRILAPRN 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LOPPARGHAHDGOALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 POILVHPQDQLFQGPG-PARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
17.0%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels
                                                                                   STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/09/991,326
FILING DATE: 21-No. 6395872-2001
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 19-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
TELECRANOMINICATION INFORMATION:
TELECRANINICATION INFORMATION:
TELECRANIS 617-542-8906
                      Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-991-326-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 XTYMCVATNSAGHRESRAARVSIQEP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 GIYTCVATNILGKVEAQ-VRLEVKDP 539
                        ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-752-307B-12
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Sequence 13, Application US/08752307B
Sequence 13, Application US/08752307B
Patent No. 5952171
GENERAL INFORMATION:
APPLICANT: Gearing, David A.
APPLICANT: Gearing, David B.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 LVIMNP-----TKAQDAGVYQCLASNPVGTVVSREAILRFGFLQE-FSKEERDPV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 -AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEX 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 KAHEGWGVMLPCNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTTGNLYIARTNASDLG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 TYMCVATNSAGHRE----SRAARVSIQ------EPQDYTEPVELLAVRIQLE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 NYSCLATS---HMDFSTKSVFSKPAQLNLAAEDTRLFAPSIKARFPAETYALVGQQVTLE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 EDOPLSVI-PPEESTEE---QVILLACRARASPPATYRWKMNGTEMKLEPGSRHQLV-GGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.5%; Score 228; DB 4; Length 607; 29.5%; Pred. No. 1.7e-14; tive 38; Mismatches 99; Indels
                CURRATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991.326
FILING DATE: 21-No. 6395872-2001
APPLICATION NUMBER: 08/752,307
FILING DATE: 19-NOV-1996
ATTOREY/ABRI INFORMATION:
REGISTRATION NUMBER: 35,283
REFRENCE/DOCKET NUMBER: 09404/02002
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 NVTLLNPDPAEGPKPRPAVWLXW-KVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFAFGNPVPR-----IKWRKVDG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-991-326-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 607 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29....
Rest Local Similarity 29....
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-752-307B-13
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Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEX 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 KAHEGWGVMLPCNPPAHYPGLSYRWLINEPPNFIPTDGRHFVSQTTGNLYIARTNASDLG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 NYSCLATS---HMDFSTKSVFSKPAQLNLAAEDTRLFAPSIKARFPAETYALVGQQVTLE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%; Score 228; DB 4; Length 607; 29.5%; Pred. No. 1.7e-14; tive 38; Mismatches 99; Indels
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: Windows95
SOFTWARE: FascERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-No. 6391586-2000
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
RRGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 NVTLLNPDPAEGPKPRPAVWLXW-KVSG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 CFAFGNPVPR-----IKWRKVDG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 607 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                         APPLICATION NUMBER: 08/752,307
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09991326
Patent No. 6395872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
COUNTR: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                        FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.5%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-707-802-12
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CITY: Boston
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Patent No. 6391586

GENERAL INFORMATING.

APPLICANT: McCarthy, Sean A.

Gearing, David P.

Levinson, Douglas A.

TITLE OF INVENTION: MCCDING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YMCVATN-----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | : : | | : :| | : :| | XTCVVTSTVTNARVLGSPTPLVLRSDGVMGEYEPKIELQFPE--TLPA-AKGSTVKLECF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V-VGEQFTLECGPPWGHPEPTVSW-WKDGKPLALQPGRHTVS--GGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 PVFVKEPSNSIFPVGSEDKKITLNCEARGNPSPHYRMQLNGSDID-TSLDHRYKLNGGNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 POILVHPODOLFOGPGPAR --- MSCRASGOPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 219; DB 2; Length 59
28.2%; Pred. No. 1.4e-13;
tive 39; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 TLLNPDP-----AEGPKPRPAVWLXWKVSGPXRLPNLTRPCSG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ALGNPVPQINWRRSDG-MPFPTKIKLRKFNGVLEIPNFQQEDTG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFFWARE: FREESEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                 09404/020001
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,307B
FILING DATE: 19-NOV-1996
                                                                                                                                                               Anita L.
                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anit.
REGISTRATION UNDRER: 35,283
REFERENCE/DOCKET UNDRER: 0940
TELECOMMUNICATION INFORMATION:
TELEFAK: 617-542-8906
TELEK: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.29
                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-752-3078-13
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-707-802-13
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Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 IVINPNR------NWDTGSYQCFAINSLGTIVSREAKLQPAYL-ENFKSRMRSRVS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 YTCVVTSTVTNARVLGSPTPLVLRSDGVMGEYEPKIELQFPE--TLPA-AKGSTVKLECF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 V-VGEOFTLECGPPWGHPEPTVSW-WKDGKPLALQPGRHTVS--GGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 PVFVKEPSNSIFPVGSEDKKITLNCEARGNPSPHYRWQLNGSDID-TSLDHRYKLNGGNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PQILVHPQDQLFQGPGPAR----MSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 TLLNPDP-----AEGPKPRPAVWLXWKVSGPXRLPNLTRPCSG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 ALGNPVPQINWRRSDG-MPFPTKIKLRKFNGVLEIPNFQQEDTG 292
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OPERATING SYSTEM: Windows95
SOFTWARE: FastESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
14.8%; Score 219; DB 4; L
Best Local Similarity 28.2%; Pred. No. 1.4e-13;
Matches 80; Conservative 39; Mismatches 119;
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
APPLICATION NUMBER: US/09/707,802
                                                                                                                                            FILING DATE: <Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-707-802-13
                        FILING DATE: 07-No. 6391586-200
CLASSETECATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09991326; Patent No. 6395872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McCarthy, Sean A. Gearing, David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 IVINPNR-------NWDTGSYQCPATNSLGTIVSREAKLQPAYL-ENFKSRMRSRVS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 V-VGEQFTLECGPPWGHPEPTVSW-WKDGKPLALQPGRHTVS--GGSLLMARAEKSDEXT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 PVFVKEPSNSIFPVGSEDKKITLNCEARGNPSPHYRWQLNGSDID-TSLDHRYKLNGGNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 POILVHPODOLFOGPGPAR---MSCRASGOPPFIIRWLLNGOPLSMVPPDPHHLLPDGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%; Score 219; DB 4; Length 596; 28.2%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 TLLNPDP-----AEGPKPRPAVWLXWKVSGPXRLPNLTRPCSG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative 39; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: 24-MAY-1995
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
FILING DATE: 21-NO. 6395872-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
FILING DATE: 19-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: MELING OF STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: HOUSE RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE;
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | LENGTH: 596 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-991-326-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 80; Conserva
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57 PDGTLLLLQPPARGHAHDGQALST -- DLGVYTCEASNRLGTAVSRGARLSVAVLREDFQI 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRW-----LLNGQPLSMVPPDPHHLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 BEPPRFIREPKDQIGVSGGVASFVCQATGDPKPRVTWNKKGKKVNSQRFETIDFDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1501;
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APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
UNDBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| : :|::|: | ||||||| | | : :: 190 GALQIESSEETDQGKYECVATNSAGVRYSSPANLYVR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.8%; Score 218.5; DB 2; Best Local Similarity 30.9%; Pred. No. 5.6e-13; Matches 67; Conservative 37; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
                                                                                                                          7683-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,679
  08/130,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800
; GENERAL INFORMATION:
                      FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTAL.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE: IBM PC COMPATIBLE
                                                                                                                                                                TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-447-464-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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57 PDGTLLLLOPPARGHAHDGQALST--DLGVYTCEASNRLGTAVSRGARLSVAVLREDFQI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 QPRDMVAVVGEQF-----TLECGPPWGHPEPTVSWWKDGKPL--ALQPGR-HTVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 PPGFPNIDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDPSASNGRIKQLRS 189
                                                                                                                                                                                                                                                                                                                                                                      2 DSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRW-----LLNGQPLSMVPPDPHHLL 56
                                                                                                                                                                                                                                                 Query Match
14.8%; Score 218.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred. No. 5.6e-13;
Matches 67; Conservative 37; Mismatches 74; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: January 30, 2004, 15:57:51 Job time: 13.8238 secs
| TELEPHONE: 212-790-9090 | TELEPHONE: 212-869-864/9741 | TELEX: 6141 PENNIE | TELEX: 6141 PENNIE | SEQUENCE CHARACTERISTICS: LENGTH: 1501 amino acids | TYPE: amino acid | TYPE: amino acid | TYPE: amino acid | TYPE: protein | WGLECULE TYPE: protein | US-08-716-679-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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Sequence Sequence Sequence Sequence Sequence Sequence

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ALIGNMENTS

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US-09-918-585A-211
US-09-978-193A-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PULLICATION NO. US20040002591A1
GENERAL INFORMATION:
JAPPLICANT: Rosen et al.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERNER: POSIGE2
CURRENT APPLICATION NUMBER: US/10/047,021
CURRENT FILING DATE: 2002-01-15
FRIOR APPLICATION NUMBER: US 60/262,066
PRIOR FILING DATE: 2001-01-18
FRIOR APPLICATION NUMBER: US 69/722,329
FRIOR FILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-04
FRIOR FILING DATE: 1997-09-05
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: US 60/058,974
FRIOR FILING DATE: 1997-09-12
FRIOR PADELICATION NUMBER: US 60/050,0112
FRIOR FILING DATE: 1997-09-12
    US-10-047-021-86
    Sequence 86, Appl
Sequence 158, Appl
Sequence 211, Appl
                                                                                                         January 30, 2004, 15:54:49; Search time 28.1244 Seconds (without alignments) 2039.494 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           1 QDSPPQILVHPQDQLFQGPG.....SGPRLPREARELRGQRRNTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUBL pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-411-224-86
US-09-796-731-158
US-09-978-255-211
US-09-978-123A-211
US-09-978-123A-211
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US-09-978-585A-211
US-09-978-585A-211
US-09-978-585A-211
US-09-978-584A-211
US-09-98-134-211
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       789580 segs, 207824079 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                           US-10-047-021-86_COPY_28_303
1475
                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             protein search, using sw model
                                                                                                                                                                                                                                        BLOSUM62 .
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                             OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                        Searched:
                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
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FEATURE:
COMPLION: (274)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AVVGEQFILECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 ODSPPOILVHPODOLFOGPGPARMSCRASGOPPFTIRWLLNGQPLSMVPPDPHHLLPDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.6%; Score 1469; DB 12; Best Local Similarity 100.0%; Pred. No. 7.2e-114; Matches 276; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 WKVSGPXRLPNLTRPCSGPRLPREARELRGQRRNTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (304)
; OTHER INFORMATION: Xaa equals stop translation
US-10-411-224-86
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR APPLICATION NUMBER: 09/23,094
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR PLILNG DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1999-02-26
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1999-06-18
TWRER: 09/342,687
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FILING DATE: 1999-02-26
APPLICATION NUMBER: 60/
FILING DATE: 1999-03-01
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APPLICATION NUMBER:
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ORGANISM: Homo sapiens
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                                                                                                               FEATURE:
NAME/KEY: SITE
LOCATION: (267)
                                      NAME/KEY: SITE
LOCATION: (203
                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
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                        FEATURE
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PZ016P1
                                                                                                                                                                                                         LOCATION: (274)
COTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86
                                         NAME/KEY: SITE
LOCATION: (203)
OTHER INFORMATION: Xaa equals any amino acid
LOCATION: (267)
OTHER INFORMATION: Xaa equals any amino acid
OTHER INFORMATION: Xaa equals any amino acid
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CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/722,329
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 1999-03-04
PRIOR PILING DATE: 1999-03-04
PRIOR PILING DATE: 1999-03-04
PRIOR PILING DATE: 1997-09-05
PRIOR PLING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/057,663
PRIOR PLING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR PLING DATE: 1997-09-05
PRIOR PLING DATE: 1997-09-12
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PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 206
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
LENGTH: 304
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Publication No. US20030166906A1
GENERAL INFORMATION:
  ORGANISM: Homo sapiens
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### WOOD, WILLIAM I.
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### WOOD, WILLIAM I.
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### CURRENT APPLICATION NUMBER: 09/918.85
### APPLICATION NUMBER: 09/918.85
### APPLICATION NUMBER: 09/918.85
### APPLICATION NUMBER: 09/01.07-30
### RIOR PILING DATE: 1997-10-17
### RIOR PILING DATE: 1997-10-17
### PRIOR PILING DATE: 1997-11-03
### PRIOR PILING DATE: 1997-11-03
### PRIOR PILING DATE: 1997-11-21
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### PRIOR PILING DATE: 1998-03-10
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### PRIOR PILING DATE: 1998-03-11
### PRIOR PILING DATE: 1998-03-12
### PRIOR PILING DATE: 1998-03-13
#### PRIOR PILING DATE: 1998-03-13
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-26
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FILING DATE: 1998-03-27
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                         Ferrara, Napoleon
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Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                     Filvaroff, Ellen
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                     Botstein, David
                                                                                                                                                                                                                                                                                                                                Goddard, Audrey
                                                                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan, James
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGT
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Best Local Similarity 98.8%; Pred. No. 1.6e-100;
Matches 243; Conservative 1; Mismatches 2;
PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR PILICATION NUMBER: 09/365,164

PRIOR PILING DATE: 1999-07-30

PRIOR PILING DATE: 1999-09-30

PRIOR PILING DATE: 1999-09-30

PRIOR PILING DATE: 1999-09-30

PRIOR PILING DATE: 1999-09-30

PRIOR PILING DATE: 1999-12-23

PRIOR PILING DATE: 1999-12-23

PRIOR PILING DATE: 1999-12-29

PRIOR PILING DATE: 2000-02-5/514,010

PRIOR PILING DATE: 2000-03-01

PRIOR PILING DATE: 2000-03-01

PRIOR PILING DATE: 2000-05-14

PRIOR PILING DATE: 2000-06-19

PRIOR PILING DATE: 2000-06-29

PRIOR PILING DATE: 2000-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-09-796-753-158
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APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
                                     FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
                                                                       APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080165
APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
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LING DATE: 1998-04-15
PLICATION NUMBER: 60/081952
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APPLICATION UNMBER: 60/080333
PILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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FILING DATE: 1998-04-08
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
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ICATION NUMBER: 60/081955
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FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/082704
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181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
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98.8%; Pred. No. 3.7e-100;
iive 1; Mismatches 2;
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R APPLICATION NUMBER: 60/084627

R APPLICATION NUMBER: 60/084643

R APPLICATION NUMBER: 60/084643

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/08538

R FILING DATE: 1998-05-13
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PRIOR PELLOATION NUMBER: 60/08580
PRIOR FILING DATE: 1998-05-15
PRIOR PELLOATION NUMBER: 60/08573
PRIOR PILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08573
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PILING DATE: 1998-05-06
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
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FILING DATE: 1998-05-13
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Best Local Similarity 98.8°
Matches 243; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIILE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-10-16
PRIOR PAPLICATION NUMBER: 09/918585
PRIOR PLILING DATE: 2001-07-30
PRIOR PLILING DATE: 2001-07-30
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-11-03
PRIOR PELICATION NUMBER: 60/064249
PRIOR PELICATION NUMBER: 60/064249
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PLILING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-11
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PRIOR PELING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-20
                       Sequence 211, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
                                                                                                           APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bettein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Kuo, Sophia S.
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US-09-978-697-211
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PRIOR APPLICATION NUMBER; 60/080105
PRIOR APPLICATION NUMBER; 60/080105
PRIOR PELING DATE: 1998-03-31
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PRIOR PILING DATE: 1998-03-31
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R FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079920
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PRIOR APPLICATION UNMER: 60/082796
PRIOR FILING DATE: 1998-04-23
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PRIOR PILING DATE: 1000 0.
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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FILING DATE: 1998-04-08
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/082568
                    PLICATION NUMBER: 60/079689
LING DATE: 1998-03-27
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FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/082704
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                                                                     APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081203
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE PERERENCE: P2630PIC9

FURENT APPLICATION NUMBER: US/09/978,192A

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13
                                                        181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                        186 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVMLS 245
126 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMC 185
                                                                                                                                                                                                                                                                                                                                                                        Sequence 211, Application US/09978192A Patent No. US20020177553A1 GENERAL INFORMATION:
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R PAPLICATION NUMBER: 60/077641
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/077649
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/07791
R FILING DATE: 1998-03-12
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Grimaldi, J. Christopher
Gurney, Austin L.
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FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman
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Pred. No. 3.7e-100;
1; Mismatches 2;
                    R APPLICATION NUMBER: 60/083496
R FILING DATE: 1998-04-29
RR RILING DATE: 1998-04-29
RR APPLICATION NUMBER: 60/08354
RR APPLICATION NUMBER: 60/083554
RR APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/084598
FILING DATE: 1998-05-07
FILING DATE: 1998-5-07
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APPLICATION NUMBER: 60/084441
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/085580
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FILING DATE: 1998-04-29
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/085573
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FILING DATE: 1998-05-15
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Best Local Similarity 98.8
Matches 243; Conservative
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FILING DATE: 1998-03-20
APPLICATION UNDER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079923
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FILING DATE: 1998-03-31
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APPLICATION WNDBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/082569
                       APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/080194
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LING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/079664
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PRIOR PELINGCATION NUMBER: 60/08136
PRIOR PELICATION NUMBER: 60/08136
PRIOR PELICATION NUMBER: 60/08132
PRIOR APPLICATION NUMBER: 60/08132
PRIOR APPLICATION NUMBER: 60/08136
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-20
PRIOR PLING DATE: 1998-05-07
PRIOR PRIING DATE: 1998-05-0

Query Match
Best Local Similarity 98.8%;
Matches 243; Conservative
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Score 1311; DB 10; Pred. No. 3.7e-100; 1; Mismatches 2;

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Length 985; Indels 0

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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PLICATION NUMBER: 60/079728
LING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/078936
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FILING DATE: 1998-03-20
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/080334
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                                                                                                                                                     AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMC 180
                                                                                                                                                                                                                                         VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLX 240
                                                                                                                                                                                                                                                               VATNSAGHRESRAARVSIOEPODYTEPVELLAVRIOLENVTLLNPDPAEGPKPRPAVWLS 245
                                                                    LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
                                                                                                         LLLLGOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 125
                                                                                                                                                                                             126 AVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMC 185
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630PIC63
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CURRENT FILING DATE: 2001-10-24
PRIOR PEDICATION NUMBER: US/918585
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-03
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PRIOR PILING DATE: 1997-11-13
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Gurney, Austin L.
Hillan, Kenneth J
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PILING DATE: 1998-03-11
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, Audrey
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Paoni, Nicholas F
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Kuo, Sophia S.
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DR APPLICATION NUMBER: 60/082704
DR FILING DATE: 1998-04-22
DR PILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082004
DR PILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082700
DR PILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/08797
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/083336
DR FILING DATE: 1998-04-27
DR FILING DATE: 1998-04-27
DR APPLICATION NUMBER: 60/083322
DR APPLICATION NUMBER: 60/083322
DR PILING DATE: 1998-04-28
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R APPLICATION NUMBER: 60/083558
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R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/084637

R FILING DATE: 1998-05-07

R PILING DATE: 1998-05-07
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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083499
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083545
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/084366
R FILING DATE: 1998-05-05
R APPLICATION NUMBER: 60/08414
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/08444
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APPLICATION UNDAER: 60/085338
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/084643
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FILING DATE: 1998-04-21
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APPLICANT: Williams P. Mickey
APPLICANT: Williams P.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT PILING DATE: 2001-01-5:
PRIOR PILING DATE: 2001-01-0-15:
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
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                                                                        Length 985;
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                                                                        88.9%; Score 1311; DB 10;
98.8%; Pred. No. 3.7e-100;
iive 1; Mismatches 2;
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Filvaroff, Ellen
Fong, Sherman
Gao, Wal-Qiang
Gerber, Hanspeter
Geritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                      Query Match 88.9
Best Local Similarity 98.8
Matches 243; Conservative
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Eaton, Dan
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246 WKVSGP 251
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PRIOR APPLICATION NUMBER: 60/08152
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PRIOR APPLICATION NUMBER: 60/08256
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PRIOR PLING DATE: 1998-04-12
PRIOR PLING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082704
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08453
PRIOR PLING DATE: 1998-05-07
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61 LLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV 120
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERSINCE: P2630PLC15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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                                                            - See File Wrapper or Palm
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Pred. No. 3.7e-100;
1; Mismatches 2;
   CURRENT APPLICATION NUMBER: US/09/978,608A CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624 Prior Application removed - See File Wrapper SEQ ID NO 211 LENGTH: 985
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Grimaldi, J. Christopher
Gurney, Austin L.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Best Local Similarity 98.8
Matches 243; Conservative
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Gao, Wei-Qiang
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US-09-978-608A-211
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
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Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2;
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR PLICATION NUMBER: 60/08574
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Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
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Paoni, Nicholas F.
Roy, Margaret Ann
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Filvaroff, Ellen
Fong, Sherman
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Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049
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R APPLICATION NUMBER: 60/081195
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R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079786
R FILING DATE: 1998-03-27
R FILING DATE: 1998-03-30
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R APPLICATION NUMBER: 60/079920
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R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
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R APPLICATION NUMBER: 60/080333
R FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/078936
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-03-11
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                                                                                                                                                               Score 1311; DB 11; Length 985;
Pred. No. 3.7e-100;
1; Mismatches 2; Indels 0
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 211
LENGTH: 985
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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Publication No. US20030050239A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Pani, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Crewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E
Goddard, Audrey
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Botstein, David
Desnoyers, Luc
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                                                                                                                                                                  Query Match 88.9
Best Local Similarity 98.8
Matches 243; Conservative
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                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-211
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US-09-978-191A-211
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR PLING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/079786
PRIOR APPLICATION NUMBER: 60/079786
PRIOR PILING DATE: 1998-03-27
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PRIOR PILING DATE: 1998-03-30
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PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/081195
PRIOR APPLICATION NUMBER: 60/081203
PRIOR APPLICATION NUMBER: 60/081203
PRIOR PILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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FILING DATE: 1998-04-15
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                                     ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
                                                                                  SerileGinGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
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PRIOR FILING DATE: 2001-07-30
PRIOR PELING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
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Patent No. US20020169284A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, Audrey
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APPLICANT: Baker Kevin P.
APPLICANT: Bettein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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1998-04-08 NUMBER: 60/081049 1998-04-08 NUMBER: 60/081071 1998-04-08 NUMBER: 60/081203 1998-04-09 NUMBER: 60/081229 1998-04-09 1998-04-09 1998-04-09 NUMBER: 60/081259 1998-04-09 NUMBER: 60/081259 1998-04-09 NUMBER: 60/081259 1998-04-15		8
ILING DATE: PPLICATION ILING DATE:	PELLING DATE: PELICATION ILLING DATE: PELICATION ILLIN	AND
PRIOR	<u> </u>	PRIOR PRIOR

NUMBER: 60/084600	1998-05-07	NUMBER: 60/084627	1998-05-07	NUMBER: 60/084643	1998-05-07	NUMBER: 60/085339	1998-05-13	NUMBER: 60/085338	1998-05-13	NUMBER: 60/085323	1998-05-13	NUMBER: 60/085582	1998-05-15	9	1998-05-15	NUMBER: 60/085689	1998-05-15	NUMBER: 60/085579	1998-05-15	NUMBER: 60/085580	1998-05-15	NUMBER: 60/085573	1998-05-15	NUMBER: 60/085704	05-	NUMBER: 60/085697	
APPLICATION N	FILING DATE:		FILING DATE:	APPLICATION N	FILING DATE:		FILING DATE:	APPLICATION N	FILING DATE:	APPLICATION N	FILING DATE:	APPLICATION N	FILING DATE:		FILING DATE:		FILING DATE:	APPLICATION N									
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Alignment Scores:			
Pred. No.:	2.9e-136	Length:	3716
Score:	1550.00	Matches:	292
Percent Similarity:	98.65%	Conservative:	1
Best Local Similarity:	98.32%	Mismatches:	ღ
Query Match:	96.398	Indels:	-1
DB:	10	Gaps:	0

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(1-303)
-10-047-021-86

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4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeulleMet 23	
-	GGAGGAGACAGCCTCCTGGGGGGGGGGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60	
24	GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43	
61	GGAGGCATGGCTCAGGACTCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGTGTTC 120	
44	GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThr11e 63	
121	CAGGCCCTGCCCTGCCAGGATGAGCTGCCAAGGCTCAGGCCAGCCA	
64	ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProAroAspProHisHisLeuLeu 83	
181	GCTGGTTGCTGAATGGGCAGCCCCTGAGGATGGTGCCCCCCAGACCCACACCCTCCTG 240	
84	ProAspGlyThrLeuLeuLeuClnProProAlaArgGlyHisAlaHisAspGlyGln 103	
. 241	CCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAG 300	
104	AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123	
301	GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCA 360	
124	ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143	
361	GTCAGCAGAGAGGCGCTCGGCTGTCTGTCCTCCCGGGAGGATTTCCCAGATCCAGCCT 420	
144	ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163	
421	CGGGACATGGTGGTGGGTGAGTAGTAGTTTACTCTGGAATGTGGGCCCCCTGGGGC 480	
164	HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183	
481	CACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGGAAACCCCCTGGCCCTCCAGCCCGGGA 540	

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P263-091C11 CURRENT APPLICATION NUMBER: US/09/978,295A
                                                                                                                                        CURRENT FILING DATE: 2001-10-15

PRIOR PAPLICATION NUMBER: 60/062260

PRIOR PAPLICATION NUMBER: 60/064249

PRIOR PILING DATE: 1997-10-17

PRIOR PAPLICATION NUMBER: 60/064249

PRIOR PAPLICATION NUMBER: 60/064311

PRIOR PAPLICATION NUMBER: 60/064311

PRIOR PAPLICATION NUMBER: 60/07450

PRIOR PAPLICATION NUMBER: 60/077632

PRIOR PAPLICATION NUMBER: 60/077641

PRIOR PAPLICATION NUMBER: 60/079664

PRIOR PAPLICATION NUMBER: 60/079667

PRIOR PAPLICATION NUMBER: 60/07967

PRIOR PAPLICATION NUMBER: 60/07967

PRIOR PAPLICATION NUMBER: 60/079920

PRIOR PAPLICATION NUMBER
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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
Williams, P. Mickey Wood, William I.
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                                                                         AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
                                                                                                       141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 AGACCGGGGGGGGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCGCCTGCCCAATCTTAC 879
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       280 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC
                                                                                                                                                                                                                                                                                                460 ATCCAGCCTCGAGACATGGTGGCTGGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 210, Application US/09978295A Patent No. US20020156006Al GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, Audrey
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Desnoyers, Luc
Eaton, Dan
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APPLICANT: Baker Kevin P
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CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCyBArgAlaSerGlyGlnProPro
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294
      US-10-059-585-21

Sequence 21, Application US/10059585

Publication No. US20030082776A1

GENERAL INFORMATION:

APPLICANT: Ota 'Toshio

APPLICANT: Hayashi, Koji

APPLICANT: Hayashi, Koji

APPLICANT: Hayashi, Koji

APPLICANT: Sudiyama, Tetsuo

APPLICANT: Sudiyama, Tomoyasu

APPLICANT: Genuki, Tetsuji

APPLICANT: Grauki, Tetsuji

PRIOR APPLICATION NUMBER: US/10/059,590

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 21

LEMENT: LEMERAL FARESEQ for Windows Version 4.0

SEQ ID NO 21

LEMENT: LEMERAL FARESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1557.00
98.33
98.00%
96.83%
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; LOCATION: (40)...(2415)
US-10-059-585-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                       US-10-047-021-86 (1-303) x US-10-411-224-31 (1-1346)
                                                                          Gaps:
1.23e-141
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                        Percent Similarity:
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Arg11eG1nLeuG1uAsnValThrLeuLeuAsnProAspProAlaG1uG1yProLysPro 260
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                                                                                                                                                                                                                                                                                                                                                                                                           281 ArgproCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       871 CGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGAGG 930
                                                                                                                                                                                                                                                                                                                           751 CGAATTCAGCTGGAAATGTGACACTSCTGAACCCGGATCCTGCAGARGGCCCCAAGCCT 810
        221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal
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| Sequence 31, Application US/10411224
| Publication No. US20030166906A1
| GENERAL INPORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: 50 Human Secreted Proteins |
| FILER REFERENCE: PZOIGEP!
| CURRENT APPLICATION NUMBER: US/10/411,224 |
| CURRENT FILING DATE: 2003-04-11 |
| PRIOR APPLICATION NUMBER: 09/262,109 |
| PRIOR PILING DATE: 1999-03 04 |
| PRIOR FILING DATE: 1999-05 |
| PRIOR FILING DATE: 1997-09-05 |
| PRIOR PILING DATE: 1997-09-12 |
| PRIOR PILING DATE: 1998-06-22 |
| PRIOR PILING DATE: 1997-09-12 |
| PRIOR PILING DATE: 1998-06-22 |
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PRIOR APPLICATION NUMBER: US 60/058,667
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1998-06-12
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| OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
| LOCATION: (850) ... (850)
| OTHER INFORMATION: n equals a,t,g, or US-10-047-021-31
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US-10-047-'021-31

US-10-411-24-31

US-10-611-224-31

US-00-978-258-21

US-09-978-192A-210

US-09-978-192A-210

US-09-978-189-210

US-09-978-189-210

US-09-978-189-210

US-09-978-189-210

US-09-978-193A-210

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US-10-113-03A-210

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US-10-145-128A-210

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US-10-165-05A-210
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFRENCE: P2016F2
CURRENT APPLICATION NUMBER: US/10/047,021
CURRENT APPLICATION NUMBER: US 60/262,066
PRIOR FILING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 99/262,109
PRIOR APPLICATION NUMBER: PCT/US98/18360
PRIOR APPLICATION NUMBER: US 60/057,626
PRIOR APPLICATION NUMBER: US 60/057,626
PRIOR APPLICATION NUMBER: US 60/057,663
PRIOR APPLICATION NUMBER: US 60/057,663
PRIOR APPLICATION NUMBER: US 60/057,663
PRIOR PLING DATE: 1997-09-05
PRIOR PLING DATE: 1997-09-05
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-Q=/Cgn2 1/USPTO spool p/US10047021/runat_3001200-MANTCH=0.1
-LOOPCI_B - LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORB=pct -THR MAX=100
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1. /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB_seq:*
3. /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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9. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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13. /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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ORGANICH: Home Sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
INDIVIDUAL ISOLATE: 17-18 week fetus
IMMEDIATE SOURCE:
LIBRARY: Stratagene cDNA Library 936206
CLONE: Synthesis of 4 clones
FUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemon, Vance
TITLE: Molecular structure and functional
TITLE: holecular structure and functional
TITLE: cesting of human LICAM: an
TITLE: GENOMICS
VOLUME: 11
ISSUE:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                    NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMUNICATION INFORMATION:
TELEPACK: (216) 861-5582
TELEFAX: (216) 96162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )
    DATE: 1991
    RELEVANT RESIDUES IN SEQ ID NO:
US-08-341-8438-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: JUNE 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
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199.00
36.67%
26.67%
                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: irrelevant
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Best Local Similarity:
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                                                                                                                                                                                                                                                                    HYPOTHETICAL: in ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                 LENGTH:
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Search completed: January 31, 2004, 15:30:45 Job time : 83.4611 secs

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    ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
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                                                                                                        763 GTAGAGCCAGAAGGGGGAGCAGTAGCTCCTGGTGGTACTGTGACCTTGACCTGTGAAGCC
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A Method for Characterizing the
Nucleotide Sequence of LICAM and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Ray, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue STREET: 1100 Superior Avenue STREET: Suite 700 CITY: Cleveland STATE: Ohio COUNTRY: U.S.A. ZIP: 44114-2518 COUNTRY: U.S.A. ZIP: 44114-2518 COMPUTER RADABLE FORM: MEDIUM TYPE: Biskette, 3.50 inch, 720 KD MEDIUM TYPE: ACCUBED SOFTWARE: ASCII CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/341,843B FILING DATE: NO. 58722255mber 18, 1994
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Characterized Thereby
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TITLE OF INVENTION: N.
TITLE OF INVENTION: N.
Patent No. 5872225
TITLE OF INVENTION: tF
TITLE OF INVENTION: tF
TITLE OF INVENTION: tF
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APPLICANT: Stern, David M.
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: USES THEREOF
FILE OF INVENTION: USES THEREOF
FILE REPERENCE: 0575/62175
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILID DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
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                                         786 GCCTTGCAGGGCAGCCATTGG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCCACG 839
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-TrpLeu***TrpLysValSerGlyPro***ArgLeuPro-- 277
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Matches:
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                                                                                                                                                                              278 -AsnLeuThrArgProCysSer-GlyPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                     290 rgGluAlaArgGluLeuArgGlyGln 298
                                                                                                                                                                                                                                                                                                     960 TGCCTGGCCGAGAACTCACTGGGCAG 985
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; ORGANISM: BOS Taurus
US-09-638-649-2
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                TITLE: Me
TITLE: hi
JOURNAL:
                                                             VOLUME:
ISSUE:
PAGES: 4
 AUTHORS:
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550 TGCAGT---ACCATGGGGAATCCAAAACCAGCCATTTCATGGTTCAAAGATGAAACTGCA 606
                                LeuAlaLeu---GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArg 196
                                                                                            197 AlaGluLysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArg 216
                                                                                                                                                                                                                                                                                                       Vance
A Method for Characterizing the
Nucleotide Sequence of LICAM and
                                                                                                                                                                                                                                                                                                                                              Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
                                                                                                                                                         217 GluSerArgAlaAlaArgValSerIleGln 226
                                                                                                                                                                           720 Kb
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LIBRARY: Stratagene cDNA Library 936206
CLONE: C2
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APPLICATION NUMBER: US/08/427,497E
TILING DATE: April 24, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,991
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 6:
SUDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
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COMEUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: storable
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                                                                                                                                                                                                                                                     Sequence 6, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION:
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for
TITLE OF INVENTION: Nucleotide Se
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AUTHORS: Hlavin, Mary Louise
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STRANDEDNESS: single
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STATE: Ohio
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAsp 85
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Molecular structure and functional testing
human LICAM: an interspecies comparison.
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Matches:
Conservative:
Mismatches:
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                                                                                                            90 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 107
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                                                                                                                                                      ProleuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 89
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667 GGAAATGAAGCAGAAGTCAGAATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT
                                                                                         MetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeuAsnGlyGln
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                                                           US-10-047-021-86 (1-303) x PCT-US94-05277-1 (1-4608)
Mismatches:
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Sequence 12, Application PC/TUS9508493
Sequence 12, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
ITLE OF INVENTION: Novel mlk Receptor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
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12.81%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 AGCTCTGCTCAAAGCTGTGGTGCCTCCAGGTCAAATGAAGCCAAAGATCATTCGG--- 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 SerProProGlnIleLeu-----ValHisProGlnAspGlnLeuPheGlnGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrileArgTrpLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 AATAACATTCCCATAAGA-----CCCTTTGACACTCGCTACAGTACAAAGAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3398
66
35
35
86
43
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08493
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BECOMM. SCOCT A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15234A
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION OF SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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201.50
43.91%.
28.70%
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3398 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-08493-12
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67

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1063 ---TCTGGAAAGCCTGTGCCCACTGTG-----AATTGGATGAAGAATGGAGATGTGGTC 1113
                                                          239 Ala-----ValArgIleGInLeuGluAsnValThrLeuLeuAsnProAspProAla 255
                                                                                                                                 256 GluGlyProLysProArgProAlaValTrpLeu***TrpLysValSerGlyPro***Arg
                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9405277
GENERAL INFORMATION:
APPLICANT: Bruskin, Arthur
APPLICANT: Jarosz, David E.
APPLICANT: Johnson, Karen
APPLICANT: Kinzler, Kenneth W.
APPLICANT: APPLICANT: Zabrecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
NUMBER OF SEQUENCES: 2
                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Banner, Birch, McKie & Beckett
1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFRENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,141
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CHROMOSOME/SEGMENT: 18q21
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IBM PC compati
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206.00
42.80%
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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              :::|||:::
1114 ATTCCTAGT 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, B
                                                                                                                                                                                                         276 LeuProAsn 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1001 G St
CITY: Washington
STATE: D.C.
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AspleuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GlnIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGly 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysSerAspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 CTCAAGTGTGAAGTCATTGGGGAGCCCATGCCAACAATCCACTGGCAGAAGAAGAACCAACAA 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     787 GTTTCT---GGCTATCCTCCACCAAGTTTTACCTGGTTACGAGGCGAGGAAGTCATCCAA 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904 GATGATGACAGTGGAATGTATACCTGTGTTGTCACATATAAAAATGAGAATATTAGTGCC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 ProleuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 MetSerCysArgAlaSerGlyGlnProProProThrileArgTrpLeuLeuAsnGlyGln
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                      LJ 2626
                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 4608 base pairs
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 ATCAGCCGACTCCAACCG
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206.00
42.80%
27.98%
12.81%
                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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Best Local Similarity:
                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
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                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                    151 GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 TrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly--- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771 GCCTTGCAGGGCAGCCATTGGTCCTGGAGTGCATCGCCGAGGGCTTTCCCACGCCCACC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ArgLeuProAsnLeuThrArgProCysSerGlyPro----- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ArgleuProArgGluA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LeuGlyValTyrThrCyg 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------cacgeceaecracecaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceaecraceae
--CACTCTGGCTCC 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 AACGGCAACCICTACTITGCCAATGTGCTCACCTCCGACAACCACTCAGACTACATCTGC
                                                                                                                        294 TTCACCATCACGGCCAACAACAACTTTGCTCAGAGGTTCCAGGGCATCTACCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 ThrLeuLeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal----Tr
                                                                                                                                                                                                                                                                                                                135 LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal------
                                                                                                                                                                                                                            US-09-041886-24

Sequence 24, Application US/09041886

Sequence 24, Application US/09041886

Sequence 24, Application US/09041886

Sequence 24, Application US/09041886

SERVERAL INFORMATION:

APPLICANT: Rabizadeh, Bharroz

TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 p-leu***TrpLysValSerGlyPro***----
   249 GAAGAGCTGGGTGTGACCGTGTACCAGTCGCCC-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                104 AlaLeuSerThrAsp---
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                                                                                    Sequence 13, Application US/08506296B
Patent No. 6313265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Consin, Kathryn.
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: The SCRIPPS Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 ------AGCCTCAAGTGTGAGGCCAGTGGCAAGCCCGAAGTGCAGTTCCGCTGG 218
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COMPUTER: IND. PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/ACENT INFORMALL.
ATTORNEY/ACENT INFORMALL.
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34.163
REFERENCE/DOCKET NUMBER: TSRI 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937;
TELEPHONE: (619) 554-2937;
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3888 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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12..3773
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STATE: California
COUNTRY: U.S.
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Best Local Similarity:
Query Match:
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                                RESULT 9
US-08-506-296B-13
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TELECOMMUNICATION INFORMATION: TELEPHONE: 1212-080-9090 TELEPHONE: 212-080-9090 TELER: 66141 PENNIE INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 5690 base pairs TYPE: nucleic acid STRANDEDMESS: unknown STRANDEDMESS: unknown MOLECULE TYPE: DNA (genomic) FRATTRE: NAMMAKEY: CDS LOCATION: 033.5338 US-08-716-679-2	Alignment Scores: 3.91e-10	Qy 13 GlySerLeuProLeuLeuLeuLeuLleutleMetGly	Db 992 TGCCAGGCCACAGGTGACCCTAAGCCACGGGTGACC Qy 68 A8nGlyGlnProLeuSerMetValProProAspPro	Qy 126 ArgGlyAlaArgLeuSerValAlaValLeuArgGlu	Oy 157 GluCysGlyProProTrpGlyHisProGluProThr
Qy 53 CysArgAlaSerGlyGlnProProProThrIleArgTrp	Qy 126 ArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAsp 145 Db 1184 GTTCATGCGAAGCTCACCGTCCTGCAGAGGACCAGCTGCTCTGGGTTC 1234 Qy 146 MetValAlaValValGlyGluGlnPheThrLeu 156 1235 CCCAACATTGAAGGTTGAAGGTTGTAGAGCGCACACGCACACCACACGCACACGCACACGCACACACATG 1294 Qy 157 GluCygGlyProProTrpGlyHisProGluProGl		3—E 5 6 8 4 4	NUMBEK OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/08/116,679 FILING DATE: CLASSIFICATION A135 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/130,570 FILING DATE: ATTORNEY/AGENT INFORMATION: MANE: Misrock, S. Leslie REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 7683-043

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LukspPheGlnIleGlnProArgAsp 145
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------CTTCGGACA 1126
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AGATCACCTGGTTCAAGGACTTCCTG 1351
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AGCAGCTTCGGTCAGGTGCCCTGCAG 1411
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                                                                                                                                                                                                             CCTGGAACAAGAGGCAAGAAAGTG 1051
                                                                                                                                                                                                                                                                                              laHisAspGlyGlnAlaLeuSerThr 107
                                                                                                                                       InGlyProGlyProAlaArgMetSer 52
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GAGGGTGCTTGGCTGAAGAGCCACCC 931
                                                                                     lyglyMetAlaGlnAspSerProPro 32
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                                                                                                                                                                                                                                                                             89 CTCGTTGGAGGCTGTGCAGAGAGCCCCCCAGGTTTATCAAAGAACCCAAGGACCAG 148
                                                                                                                                                                                                                                                                                                                                          149 ATCGGCGTGTCGGGGCGTGTGGCCTCTTTCGTGTGTCAGGCCACGGGTGACCCCAAGCCA 208
                                                                                                                                                                                                                                                                                                                                                                                        269 TITGATGAG------AGTGCAGGGCAGTGCTGAGGATCCAGCCG----- 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 ValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlu 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
                                                                                                                                                                                              2 GlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeu
                                                                                                                                                                                                                      38 GGCCCTGGCATGGTGTCTGTGGTTGGTCCCATGGGC-----CTCCTTGTGGTCCTG 88
                                                                                                                                                                                                                                                             22 IleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGln 41
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Matches:
Conservative:
Mismatches:
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                                                                              8.31e-11
246.00
44.13%
29.84%
15.30%
STRANDEDNESS: single
              TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                              ; MOLECULE TYR
PCT-US94-10166-6
                                                                    Alignment Scores:
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872 GGTCCTGTGGGGCTCTTCCTTGTACTGCTGGCGAGGGGTGCTTGGCTGAAGAGCCACCC 931
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                                      290
                                                                          833
                                                                          ---ecrcecccaraceracaracicaarecacecccade
                                      -----SerGlyProArgLeuProArg
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: Pennie & Edmonds
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5690
72
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Conservative:
Mismatches:
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766 CGTGAACATCA-CCTGCGTGG---CCGTGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/130,570
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REPRENCE/DOCKET NUMBER: 7683-
TELEPOWNICATION INFORMATION:
TELEPAX: 212-790-9090
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                  ; Sequence 2, Application US/08447464; Patent No. 5840842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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237.50
48.07%
30.90%
                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                      279 LeuThrArgProCys
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                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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147 ValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlu 166
                                           185 ---HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
                                                                                                                                                                                572 ATCAAACAGCTGCGATCAGGAGCCCTGCAGATGAAAGCAGTGAGGAAACCGACCAGGGC 631
                                                                                                                                                                                                                                   204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223
                                                                                                                                                                                                                                                                                                            224 SerileGinGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgileGin 243
                                                                                                                                                                                                                                                                                                                                                 ------GIGCGAGICCGC 708
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                                                                                ProThrValSerTrpTrpLysAspGlyLysProLeu-----AlaLeuGlnProGlyArg
                                                                                                      632 AAATATGAGTGTGGCCACCAACAGCGCCGGCGTGCGC-------
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766 CGTGAACATCA-CCTGCGTGG---CCGTGG---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCHMIDY, AZRIEL
APPLICANT: SCHMIDY, AZRIEL
APPLICANT: SCHMIDY, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STRRET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
OPPRATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 18992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-10166-6; Sequence 6, Application PC/TUS9410166; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 138825
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
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94
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101
77
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INPOMMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
REFERENCE/POCKET UNMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
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44.13$
29.84$
15.30$
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-09-158-657-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity:
Query Match:
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Pred. No.:
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185 ---HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLyBSerAspGlu*** 203
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:09 CGAGTGACCTGGAACAAGAAGGCCAAGAAGGTCAACTCTCAGCGCTTTGAGACGATTGAG 268
                                                                                                                                                                                                           ---PheGlnIleGlnProArgAspMet 146
                                                                                                                                                                                                                                                                                                                                                                                                                                             395 CTCCGAGAGGACCAGCTGCCTCTGGCTTCCCCAACATCGACATGGGCCCACAGTTGAAG 454
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                                                                                                                                                                                                                                                                                                                                        115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
89 CTCGTTGGAGGCTGTGCAGCAGAGAGACCCCCCAGGTTTATCAAAGAACCCAAGGACCAG 148
                                                                       149 ATCGGCGTGTCGGGCGTGTGGCCTCTTTCGTGTGTCAGGCCACGGGTGACCCCAAGCCA 208
                                                                                                        77 ProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArg
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Patent No. 6214564
GENERAL INFORMATION:
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEGE, SU JANE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 ---GCTCGCCCATACGTGAAGTGGATGCAGGGGGCCGAGG
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STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 CGTGAACATCA-CCTGCGTGG---CCGTGG
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CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-158-657-6
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                                   244 LeuGluAsnValThrieuieuAsnPro------AspProAlaGluGlyPro 258
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----TACTCCTCACCTGCCAACCTCTAC---GTGCGAGTCCGC 706
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                                                                                                                                                                                                                           792 ---GCTCGCCCATGCCATACGTGAAGTGGATGCAGGGGGCCCGAGG 833
                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08800825A
Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       279 LeuThrArgProCys-----SerGlyProArgLeuProArg
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94
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101
77
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTONEY/AGENT INPOMMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
TELECOMMULCATION INPORMATION:
TELECOMMULCATION INPORMATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-047-021-86 (1-303) x US-08-800-825A-6 (1-6000)
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: J. MARK HAND - MERCK & CO., INC.
126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                  166 CGTGAACATCA-CCTGCGTGG---CCGTGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
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246.00
44.13%
29.84%
15.30%
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ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: NEW JERSEY
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Query Match:
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                                 344 Greecceagacregriege---gagareacagreeargecaagerrace----gre 394
                                                                                                 ValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlu 166
                                                                                                                                                                                        Grégregacegacaceccaccaccaccaccaccaccage---escaaccergac 511
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GlualaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
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766 CGTGAACATCA-CCTGCGTGG---CCGTGG---------
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APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: TUTLEDGE, SU JANE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
                                                                           LeuArgGluAsp-----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006F
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Patent No. 5658756
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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CORRESPONDENCE ADDRESS:
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STATE: NEW JE
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US-08-348-006B-6
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Matches:
Conservative:
Mismatches:
Indels:
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                TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEPAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
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246.00
44.13%
29.84%
15.30%
REFERENCE/DOCKET NUMBER:
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
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997 TACCAGTGCATGCCAAAGAACGTGCCCGGAGAGGTGAAGACGCAAGAGGTGACCTCAGG 1056
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790 CCCCGGATCACCTCCGAGCCCCAGGACGCAGATGTGACCTCGGGGAACACGGTGTACTTC 849
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Sequence 1132, Application US/09016434

Battent No. 6500338

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Offrey J. Seilhamer
APPLICANT: Offrey J. Seilhamer
APPLICANT: OFFRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION

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208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----cricaggacacceggargaaaccricracgagricr 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 ProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArg 96
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269 TTGATGAG-----AGTGCAGGGGGAGTGCTGAGGATCCAGCCG
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Matches:
Conservative:
Mismatches:
Indelp:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOORD PERFECT 6.1 FOr WI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37,071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4078 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
NUMBER OF SEOUENCES:
                                                                                                                                           PALO ALTO
CALIFORNIA
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; CLONE: g1407624
US-09-016-434-1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                 STATE: C. COUNTRY:
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2, Appli 1, Appli 1, Appli 2, Appli

Appl

6, Appli 1, Appli 5, Appli 5, Appli 7, Appli 1, Appli

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Run on:

Sequence:

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Sequence 72, Appl
Sequence 760, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
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Sequence 5, Appli
Sequence 7, Appli
Sequence 6, Appli
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Sequence 20, Appl
Sequence 1, Appli
Sequence 4, Appli
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Sequence 3, Appli
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Sequence 17, Appl
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Sequence 1
Sequence 2
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OTHER INFORMATION: Incyte ID No. 6426186 199882.3
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
         US-09-638-649-2
US-08-341-6438-1
US-08-341-6438-1
US-08-427-497E-2
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US-08-506-2968-23
US-08-506-2968-20
US-08-506-2968-20
US-08-620-312D-72
US-08-620-312D-72
US-09-620-312D-72
US-09-727-30-6
US-08-727-30-7
US-08-73-148-1
US-08-73-148-1
US-08-740-75
US-08-77-730-3
US-08-77-730-3
US-09-877-730-3
US-09-877-730-3
US-09-877-730-3
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US-09-877-730-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Wichael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT APPLICATION NOWBER: 12009-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-484-970B-66; Sequence 66, Application US/09484970B; Patent No. 6426186; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
! LOCATION: 1838, 5528
! OTHER INFORMATION: a, t, c, g,
US-09-484-9708-66
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276.50
38.80%
29.34%
17.20%
            TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
                                                                                                        111.9
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 Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=Cqq12_1/USFTO spool_p/US1047021/runat_30012004_145453_24595/app_query.fasta_1.910
-Q=/Cqq12_1/USFTO spool_p/US1047021/runat_30012004_145453_24595/app_query.fasta_1.910
-DB=18sued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL-LOCAL_OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINIMENS=0 -MAXLEN=200000000
-USER=US10047021_@CGN 1 1133_@runat_30012004_145453_24595 -NCFU=6 -ICFU=3
-NO MWAP -LARGEQUERY -NGG SCORES=0 -WAIT -NSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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6, Appli
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2012.290 Million cell updates/sec
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                                                                                        January 31, 2004, 12:35:25; Search time 66.4611 Seconds
                                                                                                                                              US-10-047-021-86
1608
1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-484-970B-66
US-09-016-434-1132
US-08-348-006B-6
US-08-800-825A-6
US-09-158-657-6
PCT-US94-1016-6
US-08-47-46-6
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US-09-041-886-24
PCT-US94-05277-1
PCT-US95-08493-12
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                                                                                                                                                                                                                                                                                     569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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                                                                                                                                               Title:
Perfect score:
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Maximum DB seq
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Database :

276.5 246 246 246 246 237.5 237.5 207 206 206

Result

us-10-047-021-86.rng

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Search completed: January 31, 2004, 12:48:08
Job time : 254.772 secs
                                                                                                                                                                                                                                                                                                            The invention relates to a method for modulating the amount of Comm (Commissureless) polypeptide in contact with a cell expressing active Robo (roundabout) on its surface. The method comprises modulating the effective amount of Comm polypeptide in contact with the cell, where the amount of expressed active Robo is specifically modulated inversely with the modulation of the effective amount of Comm in contact with the cell. The method is used to modulate the amount of active Robo expressed on a cell. The method can be used to screen for agents that modulate Robo:Comminteractions. This is particularly useful for modulating nerve cell
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                                                                                                                                                              C, Kid T, Mitchell KJ,
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                                                                                               14-NOV-1997;
                                                                13-NOV-1998;
WO9925833-A1
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162 TrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGln 181
                     583 CGAGGCCATCCTGAGCCCACCATTCCATGGAAGAAAGATGGCTCTCCCACTGGATGATAAA
                                                                                                                            Glu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAla
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brain cord. Interpretation was lucinitied in a number to the color of color of color of the color of the color of color of the color of the color of color of the color of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This claimed cDNA sequence, the coding region of which is also claimed, codes for novel human T85 (see AAW83927), also referred to FMHB-6D4 and FMHB-SD4. The cDNA was identified in a human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
                                                                                                                                                                                                                                                                                                                                                                            FHMB-6D4; FMHV-SD4; human; neurological disorder; therapy;
                                                                                            634 CAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 A; 1011 C; 1045 G; 1081 T; 0 other;
                                                                   284 erGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg
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958..3219
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958..1017
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P-PSDB; AAW83927.
                                                                                                                                                                                                                                                                                                                                    Human T85 cDNA
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Length: Matches: Conservative:

1.03e-19 453.00 54.51%

Percent Similarity:

Alignment Scores:

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1014 CTCCCGTCTTCGTCAGGAAGATTTTCCACCTCGCATTGTTGAACACCCTTCAGACCTGAT 1073
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modulation; nerve cell function; ds.
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  Mismatches:
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                                                                                        US-10-047-021-86 (1-303) x AAV69278 (1-4291)
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GGACATGGTGGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGCCCA 273
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of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure.

TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids and proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat cell proliferative disorders (e.g. cancer), and neurological disorders e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AspGlyThrLeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAl 104
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                    uThrargProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnAr 299
                                                                                                                                                                                                                                                                                             Human; TANGO 315; clone jthAa060g22; TANGO 330; TANGO 437; TANGO 480; cellular process regulator; gene therapy; adrenal gland; cancer; ss; Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia; cell proliferative disorder; neurological disorder; Alzheimer's disease.
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/product= "TANGO 330 form 1 protein"
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lacks a start codon"
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                                                                                                                                                                                                                                                              Human TANGO 330 form 1 cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atheroscie or menorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 resusful in gene therapy for treating a hypoxic condition such as cancer, cardiac
              Novel endothelial cell-specific molecule polypeptide 1 or 4, useful imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
                                                                                                                                                                                                              endothelial cell-specific molecule 4; ECSM4; neovasculature;
                                                                                                                                                                                                                     imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic; cardiant; gene; 88.
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medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence encodes mouse ECSM4 protein.
                                                                                                                                                                                                                                                                                                         T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3688
223
24
52
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                  BP; 801 A; 1115
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1145.50
82.06%
74.09%
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Best Local Similarity:
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comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5' end
complementary strand of a polynucleotide which comprises a 5' end
complementary strand of a polynucleotide which comprises a 5' end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3' end sequence, where the
coligonucleotide which comprises a 1' end sequence, where the
coligonucleotide of the polynucleotides and the combination of
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03165 to AAH13628 and
AAH3633 to AAH18742 represent human comba sequences; and AAH13629 to AAH13632
crepresent oligonucleotides, all of which are used in the exemplification
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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Best Local Similarity:
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by the
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                                                                                                                                                                                                                                                                                                                                                                     TCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGGAGCTTCTGGCTGTGCGAATTCAG
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         CACCCAGAGCCCACAGACTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA
                                                                                                                                                                                                                                                       Thr TyrMet CysVal AlaThr Asn Ser AlaGly His Arg Glu Ser Arg AlaArg Val
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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Otsuki
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A, Nagai K,
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T, Wakamatsu
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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Sugiyama
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The present sequence encoding for human TANGO 330 form 2 is isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA clone Jthxe181e12 from a human astrocyte cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins are useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in care useful as modulating the TANGO nucleic acids are also described. CC hiagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. CC monitor protein levels in tissue as a clinical testing procedure. CC monitor protein may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to threat cell proliferative disorders (e.g. cancer),
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                                                                                                                                                                             Isolated secreted proteins and their encoding nucleic acids are use for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
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P-PSDB; AAU00501.
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                                30-SEP-1999;
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                              AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla
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note= "The ORF is specifically claimed"
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144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163

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The present invention relates to the isolation of novel human PRO polypeptides, and the polymucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and causes bioactive molecule maybe a toxin, radiolabel or antibody, and causes bioactive molecule maybe a toxin, radiolabel or antibody, and causes capture molecule maybe a toxin, radiolabel or antibody, and causes apported immune disorders, diabetes or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system disorders, kidney disorders, cardiac insufficiency, nervous system disorders, and wound healing. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation analysis of individuals with genetic disorders, and in gene therapy. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCCAGGACCAGCTGTTC 120
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                                                                                                                       , Baker KP, Botstein D, Desnoyers L, Baton D; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3716 BP; 757 A; 1225 C; 1032'G; 702 T; 0 other;
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Best Local Similarity:
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P-PSDB; ABU61102
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Goddard A, G
Kljavin IJ,
Shelton DL,
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ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyH1sAlaH1sAspGlyGln 103

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ArgAspWetValAlaValValGlvGluGlnPheThrLeuGluCysGlyProProTrpGly
                                                                                                                                                                                HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly
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99WO-US00106.
99WO-US05028.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78997 represent PCR primers and probes used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                                                                                                                               Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
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                       30-DEC-1999; 99WO-US31243.
30-DEC-1999; 99WO-US31274.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00319.
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AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123
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                                                                                                                                                                             144 ArgAspMetValAlaValValGluGlnPheThrLeuGluCysGlyProProTrpGly
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                          ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaArgVal
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                                                                                          124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro
                                                                                                                  GTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCT
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99US-0123957.
99US-0130232.
99US-0131445.
99US-0131445.
99US-014287.
99US-0145698.
99US-0145698.
99US-01658813.
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14-MAY-1999;
23-JUN-1999;
26-JUL-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coaquiation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present invention.
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98US-008589.
98US-008569.
98US-0085670.
98US-0086023.
98US-0086392.
98US-0086392.
98US-0086414.
98US-0086486.
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P-PSDB; AAY41716.
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15-MAY-1998;
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15-MAY-1998;
15-MAY-1998;
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18-MAY-1998;
22-MAY-1998;
22-MAY-1998;
22-MAY-1998;
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Pred. No.:
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28-MAY-1998
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13-MAR-1998;
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160 CAGCTGTTCCAGGCCCTGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCCACCCT
                                                                                                                 CGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCT
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                                             ProThr1leArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis
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phosphatase; signal transduction;

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Nucleotide sequence of a human protein kinase/protein phosphatase.
                                                         Human, protein kinase, protein pho
intracellular signalling pathway,
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T, Funahashi
Location/Qualifiers
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4product= "protein kinase/protein phosphatase"
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18-JAN-2000; 2000JP-0118776.
17-FEB-2000; 2000JS-0118372.
02-MAY-2000; 2000JP-0183757.
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, Sugiyama T
, Nezu J;
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disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence encodes human ECSM4 protein.
                                                                                                                                                                                                                                                                            GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln
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                                                                                                               C; 1053 G; 698 T; 0 other;
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                                                                                                                Sequence 3715 BP; 725 A; 1239
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The present invention describes primer sets for synthesising 5602

(full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dr primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

coligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprises a 1-end sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprises a 3'-end sequence. Where the

complementary strand of a polynucleotide which comprises a form of

polynucleotide comprises at least 15 nucleotides and the combination of

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

configurally full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

configurally sithout any specialised methods. AAH03166 to AAH13628 and

AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

AAH13633 to AAH13632 to AAH13632

configuration in the exemplification

configuration.
therapy; ss.
                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                          rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg
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Otsuki
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A, Nagai K,
                                                                                                                                                                                                                                                                              Human cDNA sequence SEQ ID NO:18084
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S, Sugiyama T, Wakamatsu
                                                                                                                                                                   AAH18180 standard; cDNA; 4262
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0241899.
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                                                         The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate tags haematopoiesis e.g. to treat appliate the immune system e.g. to treat multiple sclerosis, to regulate the immune system e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. barkinson's disease. The present sequence is a coding sequence of the
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        An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                    Seguence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac
                              GCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGGAGCTTCTGGGCTGTG
                                                                                                                           241 ArgileGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro
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221 AlaArgyalSerIleGlnGluProGlnAgpTyrThrGluProValGluLeuLeuAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endometriosis; hypoxic condition; angiogenesis; cytostatic; cardiant; gene; 88.
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Human, antianaemic, vulnerary, antiinflammatory, immunomodulator,
antiinfertility, cerebroprotective, cytostatic, rheumatic, gene therapy,
neuroprotective, antiparkinsonian, protein therapy, EST;
                       GGCACGGCAGTCAGCAGAGGCGCTCGCTGTCTGTGGCTGTCCTCCCGGGAGGATTTCCAG
                                                               IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro
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   GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln
                                                                                    GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer
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, Drmanac RT;
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Yang Y, Wehrman T,
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                                                                                                                                                                                                                         New polynucleotides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or
                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (ABQ92553-ABQ92607) and proteins (ABP62013-ABP62153) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archritis and ulcerative colitis; (c) cardlovascular disorders such as myocardial ischaemias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
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                                                                                                                                Olsen
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                                                                                              (HUMA-) HUMAN GENOME SCI INC
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P-PSDB; ABP62033.
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Ebner R, Brewer LA;
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                                                                                                                                                                                                                                                                                                                                                         Lafleur DW,
Shi Y,
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Title: Perfect score: Sequence:	US-10-047-021-86 1608 1 MGSGGDSLLGGRGSLPLLLLSGPRLPREARBLRGQRRVTG 303
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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DNA encoding a human secreted protein. AAX51721 standard; DNA; 1346 BP. 17-JUN-1999 (first entry) AAX51721; AAX51723

ALIGNMENTS

Human secreted protein; cancer; immune disorder; infection; inflammatory disorder; skin disorder; tuniour; abtheroselerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; peripheral neuropathy; skeletal disorder; neurological disorder; akthritic disorder; skeletal disorder; neurological disorder; transplant rejection; ss.

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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

1. 250318

1. 250318

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Conservative:
Mismatches:
Indels:
Gaps:
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Lead (15-NOV-2002) Human Genome Sequencing Center, Department Lecular and Human Genetics, Baylor College of Medicine, One Praza, Houston, TX 77030, USA

v 15, 2002 this sequence version replaced gi:23266067.

equence in this assembly is a combination of BAC based reads hole genome shotgun sequencing reads assembled using Atlas hole genome shotgun sequencing reads assembled using Atlas holy (a 'contig-seaffold'). Bach contig-scaffold, and sequence contigs are ordered and oriented, and separated add spilled with Ns to the estimated size. The sequence xend beyond the ends of the clone and there may be sequence set with a contig-scaffold that consist entirely of whole genome un sequence reads. Both end sequences and whole genome un sequence only contigs will be indicated in the feature
m.B., Mapua,P., Martin,K., Martinez,E.,
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Chang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
tock,G. and Glbbs,R.A.
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lar and Human Genetics, Baylor College of Medicine, One
aza, Houston, TX 77030, USA
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ct: hgsc-help@bcm.tmc.edu
----- Project Information
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202698 CTTTCCCTCTTAGGAGGCAAGGCTCTGGATTCTCCACCCCAGATCCTAGTTCATCCCCAG 202639
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                 Assembly program: Phrap; version 0.990329
Consensus quality: 201827 bases at least Q40
Consensus quality: 204782 bases at least Q30
Consensus quality: 208712 bases at least Q20
Estimated insert size: 209571; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-136D4"
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104879. .106665
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/note="clone_boundary
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/note="wgs_contig"
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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eavee, K., Bearland, S., Finley, M., Eugen, C., Evane, A., Francia, M., Durbin, K., Duval, B., Eavee, K., Edgan, M., Partes, L., Florer, M., Poster, P. Francia, S., Finley, M., Partes, M., Potter, P., Forer, M., Poster, P. Francia, S., Finley, M., Flang, M., Pottes, L., Florer, M., Poster, P., Ganza, M., Jang, H., Johnson, B., Holdson, M., Jolive, M., Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolive, M., Jackson, L., Lolsaged, H., Lozado, R.J., Lui, X., Mar, J., Johnson, R., Johnson, R., Johnson, M., Mallind, T., Liu, W., Lui, W., Martin, R., Martin, R., Martin, R., Martin, R., Martin, M., Ma

Center: Baylor College of Medicine Center: Baylor College of Medicine Center code: BCM Web alte: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc_help@bcm.tmc.edu .----- Project Information Center project name: GXDD Center clone name: CH230-136D4

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                                                                                                                            Insert size: 210000; agarose-fp
Insert size: 214159; sum-of-contide
Quality coverage: 10.7 in Q20 bases; sum-of-contigs
Quality coverage: 10.5 in Q20 bases; sum-of-contigs
438 5537: gap of 100 bp
538 134170: contig of 126633 bp in length
171 134270: gap of 100 bp
172 134270: gap of 100 bp
173 159037: contig of 24767 bp in length
174 159037: contig of 24767 bp in length
175 12279: contig of 53142 bp in length
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AspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro
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All repeats were identified using Ke Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/ 		10471 ARCACCCARACTINGS TO THE TOTAL	8 & 8
O'Neil, D., Oliver, J., Peterson, K., F Rachupka, A., Ramasamy, U., Raymond, C. Roman, J., Schauer, S., Schupback, R., Spencer, B., Stange-Thoman, N., Stoja Talamas, J., Tesfaye, S., Theodore, J., Wassilev, H., Venkataraman, V.S., Vie Wyman, D., Young, G., Zainoun, J., Zemb Direct Submission Submitted (23-MAR-2003) Whitehead In Research, 320 Charles Street, Cambrio M Mar 23, 2001 Athis seminone vorsion	TITLE JOURNAL	uleuleulavalargileginteugiukanvalthrieuleukanproaspproalagi 	6 6 6 6 6
Graham, L., Grand-Pierre, N., Hafez, N. Hall, J., Horton, L., Hulme, W., Illev, Kamat, A., Karatas, A., Kalls, C., Land Lindblad-Toh, K., Liu, G., Lui, A., Mak Macdonald, P., Major, J., Manning, J., Meldrim, J., Meneus, L., Mihova, T., On Nguyen, C., Nicol, R., Norbu, C., On O'Neil, D., Oliver, J., Peterson, K., P.,	·	GAATACTCCAGAGCTGAAAACTCTGGGGAGCCAAGTTTGTCCACGATGAAGGTATGTTCCA 	5 6 6 6 6
Anderson, S., Arachi, H.M., Barra, N. Boguslavkiy, L., Boukhgalter, B., Cama Collymore, A., Cooke, P., Cox Diaz, J. S., Dodge, S., Dooley, K., Dorre Ferreira, P., FitzGerald, M., Gage, D.,		GTTAGTGTGGTCACCAGGTATGGAGTTTGGGGTCCAAGTGATGAGGCCAAATGGGCATAG	8 8 8
Direct Submission Submitted (20-DEC-2002) Whitehead In Research, 320 Charles Street, Cambri 3 (bases 1 to 214559) Birren B. Nushaum C. Lander R. Ab	TITLE JOURNAL REFERENCE AUTHORS	10051 AAAAATAAGATAGAGATCAATAATAAGGGAAGACTCTGTTGTCAACGCTTACTCACATAC 10110 226 226 10111 ATGCATATAAACACGCACTTAACCCCACACTCAAAGTTCAAGGTAAGGTAAGAACTCCA 10170	8 8 8
Seaman, S., Severy, P., Smith, C., Sper Stojanovic, N., Talamas, J., Tesfaye, S Travers, M., Vassliev, H., Viel, R., V		9991 GCTAACCAGACAGTCTACACAGTGAGTTCCAAGTTCAGTGAAAGACCTTGTCTCA 10050 226 226	8 &
Mlenga, V., Murphy, T., Naylor, J., Nay Norman, C.H., O'Connor, T., O'Donnell, Peterson, K., Phunkhang, P., Pierre, N.		9931 TGACAGTGAATGTCGATCCCAGTGCCGATGTGGAGAACAGACAG	음 & 8
Faro, S., Ferreira, P., FitzGerald, M., Gardyna, S., Gord, S., Graham, L., Grat Hagos, B., Horton, L., Hulme, W., Iliev Kamat, A., Karatas, A., Kells, C., Land Lindblad-Toh, K., Liu, G., MacLean, C., Matthews, C., McCarth, M., Maldrim, T.		226 226 9871 GGTGCTGGCTTCACATACGTGAAGATCAAGTTCTCCCAGCACTCATAAAAAGCAGAGTG 9930 226 226	888
Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 9, clone RP2 Unpublished 2 (bases 1 to 214559) Birren, B., Nusbaum, C., Lander, E., Al Barna, N., Bastien, V., Bloom, T., Bogu Camarta, J., Chang, J., Chazaro, B., Cook, A., Cook, P., DeArellano, K.	AUTHORS TITLE JOURNAL REFERENCE AUTHORS	206 tCysValAlaThrhanSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGl 226 ::: :::	8686
AC138284.3 G1:29164640 HTG; HTGS PHASE1; HTGS DRAFT. Mus muscullus (house mouse) Mus muscullus Eukaryota; Metazoa; Chordata; Cranie Mammalla; Eutheria; Rodentia; Sciurc	VERSION KEYWORDS SOURCE ORGANISM	9631 CCACCCTCCAACCTCTAAGCTTCTCAAATTGAAGACTTCATGGAGTATCTGAACCTGACA 9690 187 -ValSerGlyGlySerLeuLeuMetAlaArgAlaGluLy8SerAspGlu***ThrTyrMe 206	8 & 8
AC138284 Mus musculus SEQUENCE, 5 AC138284	Ф н	185 185 9571 CAATCCTGGGAACTCCTTTGCCCATACATCATCCTGTCCTGGGCACATTGAGCAACTGAC 9630 186Thr 186	8 8 8
286 ProArgLeuProArgGluAlaArgGluLeuArgG 	99 Db	171 TrpTrpLy8AspGlyLy8ProLeuAlaLeuGlnProGlyArgHis	& 8

Abouelleil, A., Allen, N.,

Camarata, J., Chang, J., Choepel, Y.,

Corum, B., DeArellano, K.,

Dorris, L., Erickson, J., Faro, S.,

D., Galagan, J., Gardyna, S.,

E., Magoplan, D., Hagos, B.,

E., N., Hagoplan, D., Hagos, B.,

E., J., Johnson, R., Jones, C.,

Landers, T., Levine, R.,

Mabbitt, R., MacLenn, C.,

Mabbitt, R., MacLenn, C.,

Manga, V., Murphy, T., Naylor, J.,

Menga, V., Murphy, T., Naylor, J.,

Connor, T., O'Donnell, P.,

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Connor, R., Severy, P., Smith, C.,

R., Seaman, S., Severy, P., Smith, C.,

J.J., Topham, K., Travers, M.,

Viel, R., Vo, A., Wilson, B., Wu, X.,

Viel, R., Vo, A., Wilson, B., Wu, X.,

Zembek, L., Zimmer, A. and Zody, M. DNA linear HTG 23-MAR-2003 23-356D13 map 9, WORKING DRAFT Ali,A., Allen,N., Anderson,S.,
Boguslavkiy,L., Boukhgalter,B.,
Choepel,Y., Collymore,A.,
Lingar, K., Boliza,J.S., Dodge,S.,
(M., Gage,D., Galagan,J.,
Iiw, Gage,D., Galagan,J.,
Iiw, Johnson,R., Hafez,N.,
Iiw, Macdonald,P., Major,J.,
Myowen,C., Nicol,R., Major,J.,
Nguyen,C., Nicol,R., Norbu,C.,
Nguyen,C., Nicol,R., Norbu,C.,
Raymond,C., Retta,R.,
A.N., Schauer,S., Schubback,R.,
Spencer,B., Stange-Thomann,N.,
Spencer,B., Stange-Thoma iata; Vertebrata; Euteleostomi; rognathi; Muridae; Murinae; Mus. Institute/MIT Center for Genome ridge, MA 02141, USA ion replaced gi:28460994. RepeatMasker: Institute/MIT Center for Genome ridge, MA 02141, USA IT Center for Genome Research 4/RepeatMasker.html |||||||||| TGGACAGAGG 10632 gGlyGlnArg 299 P23-356D13

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            Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 4, 2003 this sequence version replaced gi:28201704.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Seaman, S., Severy, P., Smith, C.
                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gups between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                         2271 38270: contig of 38270 bp in length 38370: gap of 100 bp 39590: contig of 1220 bp in length 39590: contig of 1220 bp in length 39590: gap of 100 bp 47274: contig of 7484 bp in length 47174: contig of 7484 bp in length 47275 61618: contig of 1434 bp in length 619 61718: gap of 100 bp 61718: gap of 100 bp 7719 86099: contig of 24381 bp in length 86199: gap of 100 bp 7700 112606: contig of 26307 bp in length 5200 112606: gap of 100 bp 770713 12606: gap of 100 bp 770713 179263: contig of 29749 bp in length 7707201 179263: contig of 29749 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9271 AGATAGAGGGCAAGGAAGTGGTAGAGCAGAATTGGGTAAGCATGTTCGGATAAGCCATC 9330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 HisAspGlyGln---AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsn 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisBroGluProThrValSer 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ProProThr11eArgTrpLeuLeuAanGlyGlnProLeuSerMetValProProAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 AspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro
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37.99%
33.77%
52.58%
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Dipublished

Stren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Canpoiano, A., Chang, J., Chazaro, B., Cooke, Y., Conargelo, M., Collins, S., Collymore, A., Cook, A., Cooke, Y., Dodge, S., Farc, S., Ferreira, P., Pitzhugh, W., Galagan, J., Garad-Pierre, N., Farzeira, P., Pitzhugh, W., Galagan, J., Garad-Pierre, N., Hagos, B., Hadford, A., Morton, L., Halme, W., Ilav, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Lawocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McLean, C., Macdonald, P., Major, J., Morpheters, R., Meldrim, J., Morbu, C., Norman, P., McKernan, K., McPheeters, R., Meldrim, J., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neal, D., O'Neal, D., O'Neal, D., O'Neal, D., O'Neal, D., O'Neal, D., O'Donnell, P., O'Connor, R., Schupback, R., Schuers, S., Schupback, R., Seberti, M., Roy, A., Santos, R., Schuers, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strawers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, E., Wayman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Subramaina, A., Travis, M., Trigillo, J., Young, G., Charles, M., Trigillo, J., Young, M., Jan, M., M., Wayman, D., Ye, W.J., Young, G., Charles, M., Subraman, M., Subraman, M., Zambek, L., Zamo, M., A., Wang, M., A., Wa
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Mus musculus clone RP24-325P4, WORKING DRAFT SEQUENCE, 9 unordered
  261 ArgProAlaValTrpLeu***TrpLygValSerGlyPro***-ArgLeuProAsnLeuTh 280
                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                          280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
                                                                                                                                                                                                                                                                                                                    ArglleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro
                                                                                                               Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-325P4
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Mus musculus (house mouse)
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AC105958.6 GI:28827995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 HisteuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology, cDNA library construction and clone selection: Kazusa DNA Research
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Published Only in Database (2002)
2 (bases 1 to 4694)
Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
Submitted (21-JAM-2002) Takahiro Nagase, Kazusa DNA Research
Institute, Department of Human Gene Research; 1532-3, Yana,
Kasarau, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,
                                                                                                                                                                                                                                                           SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243
                                                                                                                                                                                                                                                                                                                                                   LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
                                                                                                                                                                                                                                                                                                                                                                                                                                          264 ValTrpLeu***TrpLy8ValSerGlyPro***-ArgLeuProAsnLeuThrArgProCy 283
422 TCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAG 481
                                                                                                                    302 AGGCACACAGTGTCCGGGGGGATCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG 361
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The nucleotide sequence of a long cDNA clone isolated from human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/codon start=1
/evidence=not experimental
/product="FLJ00236 protein"
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/note="vector:pBluescriptII SK plus"
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Homo sapiens mRNA for FLJ00236 protein.
AK074163

    .4694
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="FLJ00236"
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Emall: Ggapbs-r@mail.nih.gov
Contact: MGC help desk
Emall: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CADORA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailue, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 34 Row: a Column: 19.
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                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3467)
                                                                                                                                                                                     Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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LUMPODOLLGGSGPAKMSCRASGQPLPTIRWILMGQPLSMATPDLHYLQSDGTLLLHR
PPTHGRPQDDQNILSALIGYTCEASNRLGTAVSRGARLSVAVLQEDSTROPROTVAV
VGESLVLECGPPWGYPKPSVSWWKDGKPLVLQPGKRTVSGDSLMVARARKNDTGTVMO
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LDGRRSLISWDPRSPGVPLLPDTSTFYGSLIAEQTSSPPVRPSPGTPAARRLPPKLTG
TSSPWASSDSLCSRRGLCSPRWSLAPAEAWKAKKKQELHQANSSPLLQGSHPMEIWAW
                                                                                                                                                                                                                     GAPSHDPQSQCVEKLQAPSSDPLPAAPLSVLNSSRPSSPQASFLSVPSPGSSNLSSSS
LASLEEEDGOSVLTPERVALCLISLSOGEETPTNSVSPANPRAPSPPATVGYISIPTSSG
LADMCRAGGGVGSEVORILCPPRICPTPTPSEGSLANGMGSASEDNVPSARASLVSSS
DGSFLADAHFARALAVAVDSFGFSLEPREADCVFTGMMARPPPLEWT"
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/gene="Robo4"
/note="Region: IGc2"
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/note="polymorphism"
/replace="a"
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/gene="Robo4"
/note="cleavage s
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/gene="Robo4"
/note="Region: i
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/gene="Robo4"
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gene="Robo4"
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/gene="Robo4"
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gene="Robo4"
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gene="Robo4"
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qene="Robo4"
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gene="Robo4"
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PRI 12-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                    CAATCAGATGGGACCCTCCTGCTACATCGGCCCCCTACCCATGGACGGCCGCAAGACGAC 336
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                                                                                                                                1 TCTGGAGGAATGGGCCTCCTGGGACTAAGTGTCCTCTGCCTCTACTGCTTCTTTTCATC
                                                                                                                                                                                MetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 PheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThr
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                                                                                                                 SerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIle
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Mismatches:
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Homo sapiens, clone IMAGE:4850025, mRNA.
BC014995
BC014995.1 GI:21955407
                                Indels:
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81.61%
74.25%
70.49%
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To (bases 1 to 2886)
Roberts,K.G. and Stewart,L.M.
Roberts,K.G. and Stewart,L.M.
Direct Submission
Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England ECLA 7BE, United Kingdom
Location/Qualifiers
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ROBO4-I; similar to Homo sapiens and Mus musculus ROBO4" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla
                                                   61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis
                                                                                                                                                                                                                                                                                            GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG
                                                                                                                                                                                                                                                                                                                                                           460 ATCCAGCCTCGAGACATGGTGGCTGTGGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG
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                              GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro
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/organism="Rattus norvegicus"
/mol type="mRNA"
/db xref="taxon:10116"
1. .2886
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/product="ROBO4"
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Rattus norvegicus ROBO4
AY277635
AY277635.1 GI:30575794
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/gene="Robo4"
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30786 TICCICGAAACICCTICCCAGGICAGGCCCTGCTGCGCCCGATCTIACACGGCC 30727
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1 (bases 1 to 7.5)
1 (bases 1 to 7.7)
1 (bases 1 to 7.8)
1 (brii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for Sprithesizing full-length cDNA and use thereof Patent: JP 2002191363-A 5069 09-UUL-2002;
                                                                                                                                                                                                                                                                            PAT 17-JAN-2003
                                                                                                                          282
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JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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JP 2002191363-A/5069
09-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeulleMetGlyGlyMetAlaGlnAgpSerProProGlnIleLeuValHisProGlnAgp
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Primer for synthesizing full-length cDNA and use thereof
BD150226
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Mismatches:
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JP 2002191363-A/5069.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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BD15026
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AUTHORS
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31985 GTGGGGCAAACCTGGGTGGAGACATCTGAGCTGAATGTTCAAGGGAACATCTGAGAGGGC 31926
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Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Dublished Only in Database (2001)

2 (bases 1 to 186971)

3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

L. Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suchiro-chou,Tsurumi,Lu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorieggc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, On Mar 7, 2002 this sequence version replaced gi:13603460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32345 CCAGGAGGCAIGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTG 32286
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                                                                                                                         Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664121
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromesome="11"
/map="11q"
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Mammalia; Eutheria;
                                                                                           sapiens (human)
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                                                                                                           Homo sapiens
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Mammalia; Eutheria; Primates;
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                                                                                            /protein_id="bab55411.1"
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//db xref="GI:14042832"
//db xref="GI:14042832"
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AQSYTALFTTQTAPGGCAPMAEELLAGWGSAEL/GGLHMCGDYEFKVRESSGRARGPD
SNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSL
PPAMMTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLEQAMERATQEP
SEHGPWTLEQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLEQAMERATQEP
SEHGPWTLEQLRATIKRPEVIATCGVALWLLLLGTAVCGADARDPLDGRSSSSDSL
SRSPGVPLLPDTSTFYGSIIAELPSSTFARFSPQVPAVRRLPPQLAQLSSPCSSSDSL
CGRRGLSSPRLSIAPAEMKAKKGGELPHANSSPLLRAGGHSLELRACELGNRGSSKNIS
                                               QSPGAVPQALVAWRALGPKLLSSQMSWLLVISLQHPSFLMKLPQLRVNRPSLRWHHRL
PPPSCCQQPPSPSLAPAVPLAPRPLPSLAPAQLPVACPAPHCHPWGRIKTAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE2000034"
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                                                                                                                                                                                                                            REFERENCE
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JOURNAL
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Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4262)

2 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamateu,A., Nagai,K. and Otsuki,T. Primer for Synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 15015 09-JUL-2002;

14L Patent: JP 2002191363-A 15015 09-JUL-2002;

15 HELIX RESEARCH INSTITUTE
16 HOMO sapiens (human)
17 PU 2002191363-A/15015
18 PD 09-JUL-2002
19 O9-JUL-2002
19 O9-JUL-2002
19 C9-JUL-2002
19 SAITO, POONZBO990
10 SAITO, SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI
19 KEIICHI NAGAI,TETSUJI OTSUKI
19 CC 12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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JP 2002191363-A/15015.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
1333 c 1209 g 84
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rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg
                                                                           ArgProAlaValTrpLeu***TrpLysValSerGlyPro***-ArgLeuProAsnLeuTh
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JOURNAL
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Hovel genes encoding protein kinase or protein phosphatase ratent: WO 0109345-A 11 08-FEB-2001;
HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, KOJI HAYASHI,KAORU SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU SUGIYAMA, AI WAKAMATSU,KEIICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHASHI, HIAKI SENO, JUNICHI NEZU

OS Homo sapiens (human)
PN WO 0109345-A/11
PD 08-FEB-2001
O8-FEB-2001 WO 2000JP005060
PR 29-JUL-1909 WO 2000JP005060
PR 29-JUL-1909 JP 99P 248036,11-JAN-2000 JP 00P 118776 PR 02-MAY-2000 UP 183767,18-OCT-1999 US 60/159590 PR 17-FEB-2000 US 60/183322
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI, PI KAORU SAITO, JUNICHI NEZU
PC C12N15/54,C12N15/55,C12N9/12,C12N9/16,C12N5/10,C12N1/21 PC C12N15/54,C12N15/55,C12N9/12,C12N9/16,C12N5/10,C12N1/21 PC C12N15/54,C12N15/55,C12N9/12,C12N9/16,C12N5/10,C12N1/21 PC FH Key Location/Qualifiers
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Ota,T., Isogai,T., N
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   ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1333 c 1209 g 84
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                                                                                                                                                                                                                                                                             (1-4262)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                181
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| GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer
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                                                                                                             ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu
                                                                                                                                                                                                                IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro
                                                                                                                                                                                                                                                                                     GGCACGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                          GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT
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                                                                                                                                                                                  ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                          AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis
                                                                                CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAAACCCCCTGGCCCTC
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PWGHPEPTVSWWKDGKPLALQPCRHTVSGGSLLMARAEKSDEGTYMCVAYNVAGHRES
RAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPPAVWLSWKVSGPAAP
AQSYTALFRTQTAPGGGAPWAEELLAGWGSAELGGLHWQDDYEFKVRESSGRARGPD
SNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSL
PPANMYVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEP
SEHGPWTLEQLRATLKRPEVIATCGVALWLLLGTAVCIHRRRARVHLGPGLYRYTS
EDAIIKHRWDHSDSQWLADTWRSTSGSRDLSSSSLSSRLGADAADPLDCTRSLLSWD
SRSGVYPLLPTTSTYGGLIAELPSSTPARFSQVPAVRRLPPQLAQLSSPCSSDSL
CSRRGLSSPRLSLAPAEAWKAKKQELQHANSSPLLEGRARGCHAGAGEV
SPGAVPQALVAWRALGPKLLSSSNELVTRHLPPAAPLFPTQSQOTQPPVAPQA
PSSILLPAAPIFILSCPSPPSPSSSNSLSTSRSSLSSLGEDQDSVLTPEEV
ALCLELSGGEETPRUSVSPMPRAAPSPTTYGYLSVPTASEFTDWGRTGGGVPFKGGVL
LCPPRPCLTPTPSEGSLANGWGSASEDNAASARASLVSSSDGSFLADAHFARALAVAV
DSFGFGLEPREADCVFIDASSSPPSBSRDSIFLTPHLSLPHWEWRPDWLEDMEVSHTQRL
DSFGFGLEPREADCVFIDASSSPPSPRSSTLSPHLEPAGFAALAVAV
DSFGFGLEPREADCVFIDASSSPPSPRSSTLSPHLEPAGFAALAVAV
DSFGFGLEPREADCVFIDASSSPPSPRSSTLSPHLEPAGFAACAVAV
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/codon start=1
/protein ida="CAD34826.1"
/db_xref="GI:21438878"
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Homo sapiens magic roundabout
AP361473
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Huminiecki, L. and Bicknell, R.
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(bases 1 to 3872)

Huminiecki, L. and Bicknell, R.

In silico cloning of novel endothelial-specific genes

Genome Res. 10 (11), 1796-1806 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John Radcliffe Hospital, Oxford OX3 9DS, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/product = "magic roundabout"
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PPANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEP
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EDAILKHRMDHSDSQWLADTWRSTGSGRDLSSSSSLSSRFLGADARDPLDCRRSLLSWD
SRSFQVPLLEDTSTFYGSLIARLPSCTPARPSQVPAVRLPPGLAGLSSPCSSDSL
CSRRGLSSPRLSLAPAEAWKAKKKQELQHANSSPLLAGGHRSLELARGELGNRGSKNLS
QSPGAVPQALVAWRALGPKLLSSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQA
PSSILLPAPPIFILSPCSPPSPQASSLSGFSPASSRLSSSLSGLGEDODSVLTPEEU
ACLIESEGETTRNSVSPMPRAPSPPTYGYLSVPTASETTDMGRTGGGVGPKGGVL
ACLIESEGETTRNSVSPMPRAPSPPTYGYLSVPTASETTDMGRTGGGVGPKGGVL
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="endothelial-specific
receptor family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
chromosome="11"
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C12N15/09, A6K38/00, A61K48/00, A61P17/02, A61P17/06, A61P19/00, PC

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/mol_type="genomic DNA"
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                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                             Sequence 134 from Patent AX405719
                                                                                                                                                    AX405719.1 GI:21438877
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Catarrhini; Hominidae;
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Ggn2_1/USPTO_spool_p/US10047021/runat_30012004_145452_24562/app_query.fasta_1.910
-DB=GenEmbl -QPMT=fastap -SUFFIX==ge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US10047021_@CGN 1 1 5066 @runat 30012004 145452-24562 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPB_LOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN INDEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN INDEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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29: em vi:*
30: em htg hum:*
31: em htg jnv:*
32: em htg other:*
33: em htg mus:*
34: em htg pln:*
35: em htg pon:*
36: em htg mam:*
37: em htg vrt:*
39: em htg vrt:*
40: em htgo mus:*
41: em htgo mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. იი αα Ω 1602 1565 1565 1567 1567 1567 11262 11262 1133.5 1133.5 1133.5 1133.5 1133.5 1133.5 1133.5 1133.5 1432.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 845.5 846 Score Query Match 188.55.00 189.55.00 28.0 27.9 27.8 27.8 3894 3650 1129 4146 186971 16652 169534 2886 3467 4694 209012 214559 223269 250318 4262 4262 186971 Length 53884 53884 53884 53884 53884 53884 53884 53884 53884 53887 53 B 6 W W 6 2229 BD085988 AF182037 AF337034 AF461119 AF37035) AF06570 AF364048 AF304131 BD085986 AF0307036 AF040989 AB046788 AX556709 BD085987 AP003501 AC014298 AC008350 AF304130 AF312580 AX556703 AC105958 AC138284 AC120636 BC014995 AK074163 AK027852 AP003501 AK056544 HSDUTT1 AX714308 BD150226 ä BD160172 AF312579 AF364047 AF361473 AF041053 AF040990 AC109983 AF060570 Mus muscu AF364048 GAllus ga AF304131 Danio rer BD085986 Method of AF337036 Danio rer AF040989 Drosophil AB046788 Homo sapi AX556709 Sequence AF312580 Drosophil AX556703 Sequence AF312580 Drosophil AX556703 Sequence AF041053 Caenorhab AF312580 Drosophil BD08598 Method of AF182037 Rattus no AF337034 Danio rer BD08598 Method of AF182037 Method of AF0337034 Danio rer BD08598 Method of AF337034 Danio sapi AC014298 Drosophil AK056544 Homo sapi AF041082 Rattus no Y17793 Mus musculu BD085989 Method of AF040990 Homo sapi AF046119 Xenopus 1 AF37035 Danio rer AP003501 Homo sapi BD150226 Primer fo AY277635 Rattus no BC014995 Homo sapi AK074163 Homo sapi AC105958 Mus muscu AC138284 Mus muscu AC120636 Rattus no AC109983 Rattus no Z95705 Human DNA s AX714308 Sequence BD074325 50 human AX405719 Sequence Description 3 Homo sapi 3 Novel gen Homo sapi Primer fo

ALIGNMENTS

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R APPLICATION NUMBER: 60/081203
R FILING DATE: 1998-04-09
R FILING DATE: 1998-04-09
R PILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081955
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R APPLICATION NUMBER: 60/081817
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R APPLICATION NUMBER: 60/082804

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R APPLICATION NUMBER: 60/082804

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R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R APPLICATION NUMBER: 60/082796

R APPLICATION NUMBER: 60/08336

R FILING DATE: 1998-04-23

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

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R FILING DATE: 1998-04-29

R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/082568
R FILING DATE: 1998-04-21
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R APPLICATION NUMBER: 60/082704
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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083554
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R APPLICATION NUMBER: 60/083558
R FILING DATE: 1998-04-29
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/08152
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
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FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366
                                                     APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081049
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FILING DATE: 1998-04-29
             LING DATE: 1998-04-01
PLICATION NUMBER: 60/080333
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/08441
60/080328
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APPLICATION NUMBER: 60/084114
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APPLICATION NUMBER: 60/084637
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                                         FILING DATE: 1998-04-01
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61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 120 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262 1 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL 83 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 121 PRDMYAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL Gaps ö Length 985; Indels Score 1337; DB 11; Pred. No. 4.1e-101; 1; Mismatches 2; PRIOR APPLICATION NUMBER: 60/084639
PRIOR PILLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084630
PRIOR PILLING DATE: 1998-05-07
PRIOR PILLING DATE: 1998-05-07
PRIOR PILLING DATE: 1998-05-07
PRIOR PILLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR APPLICATION NUMBER: 60/084639
PRIOR PILLING DATE: 1998-05-13
PRIOR PILLING DATE: 1998-05-15
PRIOR PILLING DATE: 1998-05-15 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 Query Match
Best Local Similarity 98.8%;
Matches 248; Conservative 263 AVWLXWKVSGP 273 AVWLSWKVSGP 251 143 23 PRIOR PRIOR 셤 셤 a g ઠે ò ò ð ઠ

Search completed: January 30, 2004, 15:59:02 Job time : 31.8756 secs

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APPLICANT: William: P. Mickey
APPLICANT: William: P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC12
CURRENT FILING DATE: US/09/981,915A
CURRENT APPLICATION NUMBER: US/09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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RICO FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/079294
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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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                                                                                                             Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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                        Napier, Mary A.
Pan, James;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL 82
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98.8%; Pred. No. 4.1e-101;
iive 1; Mismatches 2;
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                        R FILING DATE: 1998-05-07

R APPLICATION UNMERR: 60/084643

R APPLICATION NUMBER: 60/085339

R APPLICATION NUMBER: 60/085339

R RILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 1998-05-15
APPLICATION UNMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/085700
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/084627
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth J
Kljavin, Ivar J.
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Desnoyers, Luc
Eaton, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-05-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.1
Best Local Similarity 98.8
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVWLXWKVSGP 273
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APPLICANT: Baker Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-981-915A-211
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R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195
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R FILING DATE: 1998-04-09
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FILING DATE: 1998-04-09
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082569
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FILING DATE: 1998-04-22
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FILING DATE: 1998-04-23
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FILING DATE: 1998-04-27
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FILING DATE: 1998-04-28
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PPLICATION NUMBER: 60/083495
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-30
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FILING DATE: 1998-05-05
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FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/08441
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FILING DATE: 1998-04-22
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FILING DATE: 1998-05-07
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FILING DATE: 1998-04-08
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                        ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
                                                                       FILE REFERENCE: P2630PLG65
CURRENT APPLICATION NUMBER: US/09/999, 833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PELING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-110-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-110-33
PRIOR PILING DATE: 1997-110-33
PRIOR FILING DATE: 1997-111-13
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/077649
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079663
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ILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081049
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PLICATION NUMBER: 60/077791
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60
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APPLICATION NUMBER: 60
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R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/081952

R APPLICATION NUMBER: 60/081938

R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/08268

R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/08269

R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/08269

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/08269

R APPLICATION NUMBER: 60/082704

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R APPLICATION NUMBER: 60/084637

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APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/083336
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APPLICATION UNMBER: 60/083554
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/085323
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121 PRDMYAVVGEOPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 180 83 LPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 142 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 202 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 240 9 1 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL 23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL Gaps ö 2; Indels Score 1337; DB 11; Pred. No. 4.1e-101; 1; Mismatches 2; PRIOR APPLICATION NUMBER: 60/085582
PRIOR PLING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR PLING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15 Sequence 211, Application US/09999833A Publication No. US20030054405A1 GENERAL INFORMATION: Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Query Match
Best Local Similarity 98.8%;
Matches 248; Conservative Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Roy, Margaret Ann Shelton, David L. Stewart, Timothy Ferrara, Napoleon Filvaroff, Ellen Gerritsen, Mary E Gurney, Austin L. Kenneth APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botelein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan Kljavin, Ivar J Napier, Mary A. 263 AVWLXWKVSGP 273 |||| ||||| 241 AVWLSWKVSGP 251 Kuo, Sophia S RESULT 14 US-09-999-833A-211 61 APPLICANT: APPLICANT:

Williams, P. Mickey

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R APPLICATION NUMBER: 60/064249

R FILING DATE: 1997-11-03

R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/066364

R APPLICATION NUMBER: 60/07450

R APPLICATION NUMBER: 60/077450

R APPLICATION NUMBER: 60/077632

R APPLICATION NUMBER: 60/077632

R APPLICATION NUMBER: 60/077632

R APPLICATION NUMBER: 60/077632

R APPLICATION NUMBER: 60/077631

R FILING DATE: 1998-03-11

R PRILING DATE: 1998-03-11
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R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/078936

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/078910

R PILING DATE: 1998-03-20

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R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-26

R APPLICATION NUMBER: 60/079656

R APPLICATION NUMBER: 60/079669

R FILING DATE: 1998-03-26

R APPLICATION NUMBER: 60/079669

R FILING DATE: 1998-03-27

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079669

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079689

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079683

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R APPLICATION NUMBER: 60/079786
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R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/07791
R FILING DATE: 1998-03-12
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R APPLICATION NUMBER: 60/079920
R APPLICATION NUMBER: 60/07993
R APPLICATION NUMBER: 60/080105
R APPLICATION NUMBER: 60/080105
R FILING DATE: 1998-03-31
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R APPLICATION NUMBER: 60/080107
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APPLICATION UNDRER: 60/080165
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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PRIOR FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081071
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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98.8%; Pred. No. 4.1e-101;
iive 1; Mismatches 2;
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
PRIOR APPLICATION NUMBER: 60/08580
PRIOR FILING DATE: 1998-05-15
PRIOR PELICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08574
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Sequence 211, Application US/09978564A
Publication No. US20030050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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Best Local Similarity 98.8'
Matches 248; Conservative
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Kuo, Sophia S.
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PRIOR PEDICATION NUMBER: 60/08268
PRIOR PLING DATE: 1998-04-21
PRIOR PELICATION NUMBER: 60/08269
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-17
PRIOR PLING DATE: 1998-05-17
PRIOR PPLICATION NUMBER: 60/08539
PRIOR PLING DATE: 1998-05-15
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PRIOR PETING DATE: 1998-04-22
PRIOR PETING DATE: 1998-04-22
PRIOR PELICATION NUMBER: 60/082797
PRIOR PELICATION NUMBER: 60/08332
PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/083545
PRIOR PELICATION NUMBER: 60/083546
PRIOR PELICATION NUMBER: 60/083546
PRIOR PELICATION NUMBER: 60/084414
PRIOR PELICATION NUMBER: 60/084414
PRIOR PELICATION NUMBER: 60/084414
PRIOR PELICATION NUMBER: 60/084414
PRIOR PELICATION NUMBER: 60/084639
PRIOR PELICATION NUMBER: 60/08538
PRIOR PELICATION NUMBER: 60/08538
PRIOR PELICATION NUMBER: 60/085582

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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/082700
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APPLICANT: Tummes, Danielly
APPLICANT: Tummes, Danielly
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William; P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBUCE: PESADPLICT;
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
                                                                                                                                                      181 GTYMCVAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNDDPAEGPKPRP 240
                                                                                                                                                                                                                                                                           203 XTYMCVATNSAGHRESRAARVSIOEPODYTEPVELLAVRIOLENVTLLNPDPAEGPKPRP 262
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                                                                                1 MGGMAQDSPPQILVHPQDQLFQGPGRARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL
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98.8%; Pred. No. 4.1e-101;
tive 1; Mismatches 2;
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
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Kuo, Sophia S.
Napier, Mary A.
Best Local Similarity 98.8 Matches 248; Conservative
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Botstein, David
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Eaton, Dan
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US-09-978-403A-211
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR PELING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079656
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
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PRIOR PILING DATE: 1998-03-30
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR APPLICATION NUMBER: 60/080107
PRIOR APPLICATION NUMBER: 60/080165
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR APPLICATION NUMBER: 60/080338
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080338
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081019
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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08
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R FILING DATE: 1998-09-09
R APPLICATION NUMBER: 60/081229
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PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1990-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR PILING DATE: 1990-04-15
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PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082804
                                                FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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PPLICATION NUMBER: 60/082704
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                                                181 GTYMCVAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNDPAEGPKPRP 240
                                                                                                                                                     203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262
61 LPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 120
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CURRENT PILING DATE: 2001-10-15
PRIOR PELICATION NUMBER: US/09/918585
PRIOR PILING DATE: 2001-00-15
PRIOR PILING DATE: 1200-10-17
PRIOR PILING DATE: 12097-10-17
PRIOR PILING DATE: 12097-10-17
PRIOR APPLICATION NUMBER: 60/06424
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-14
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1999-10-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
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Publication No. US20030050239A1
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/077791
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Paoni, Nicholas F.
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Hillan, Kenneth J
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10, Sophia S.
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Desnoyers, Luc
Eaton, Dan
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121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 180
                                                     61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 120
                                                                                                                                                                   203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLINPDPAEGPKPRP 262
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLCIS
CURRENT APPLICATION VUMBER: US/09/978, 585A
CURRENT FILING DATE: 2001-10-16
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Pred. No. 4.1e-101;
1; Mismatches 2;
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 98.8
Matches 248; Conservative
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Eaton, Dan
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; ORGANISM: Homo sapiens
US-09-978-585A-211
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                                                                                                                                                PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 202
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Prior Application removed - See File Wrapper or Palm SEQ ID NO 211
LENGTH: 985
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Pred. No. 4.1e-101;
1; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
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Grimaldi, J. Christopher
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
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Gao, Wei-Qiang
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Best Local Similarity 98.8
Matches 248; Conservative
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ORGANISM: Homo sapiens
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NUMBER: 60/078936 1998-03-20 NUMBER: 60/078910 1998-03-20 1998-03-20 NUMBER: 60/079294 1998-03-25 NUMBER: 60/079664 1998-03-26 NUMBER: 60/079689 1998-03-27 NUMBER: 60/079689 1998-03-27 NUMBER: 60/079689	1998- 1998- 1998- 1998- 1998- 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER 1998- NUMBER	NUMBER: 60/08119 1998-04-08 NUMBER: 60/08119 1998-04-09 NUMBER: 60/08120 1998-04-15 NUMBER: 60/08181 1998-04-15 NUMBER: 60/08181 1998-04-15 NUMBER: 60/08181 1998-04-15 NUMBER: 60/08181 1998-04-15 NUMBER: 60/08195 1998-04-21 NUMBER: 60/08256 1998-04-21 NUMBER: 60/08260 1998-04-21 NUMBER: 60/08270 1998-04-22 NUMBER: 60/08270 1998-04-22 NUMBER: 60/08270
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PRIOR PILING DATE: 1998-04-22
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PRIOR PILING DATE: 1998-04-29
PRIOR PELICATION NUMBER: 60/083495
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PRIOR PELICATION NUMBER: 60/083495
PRIOR PELICATION NUMBER: 60/083495
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-05-05
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-18
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Gaps

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Query Match 83.1%; Score 1337; DB 11; Length 985; Best Local Similarity 98.8%; Pred. No. 4.1e-101; Matches 2; Indels 0;

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APPLICANT: Pach, Nicholas F.
APPLICANT: Pach, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timoth A.
APPLICANT: Stewart, Timoth A.
APPLICANT: Stewart, Timoth A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION WUMBER: US/09/978,189
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
181 GTYMCVAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNDDPAEGPKPRP 240
                                                                                           203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 211, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Bakerazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Bate Applicant Applicant Applicant Bate Applicant Applicant Baton, Dan
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PRIOR FILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR PILING DATE: 1998-03-13
PRIOR PLING DATE: 1998-03-13
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Grimaldi, J. Christopher
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Paoni, Nicholas F.
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Goddard, Audrey
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Pred. No. 4.1e-101;
1; Mismatches 2;
                  PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08349
PRIOR PILING DATE: 1998-04-29
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PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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   APPLICATION NUMBER: 60/083495
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Best Local Similarity 98.8%;
Matches 248; Conservative
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PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
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PRIOR PILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29
                       APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-03
APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/082797
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PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080333
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LING DATE: 1998-04-08
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PPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082804
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1998-03-26
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APPLICANT: Tunnas, Daniel

APPLICANT: Willianns, P. Mickey

APPLICANT: Wood, Williann I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE FERENCE: P2630P1C63

CURRENT APPLICATION NUMBER: US/09/999, 832A

CURRENT APPLICATION NUMBER: US/09/91885

PRIOR FILING DATE: 1997-110-17

PRIOR FILING DATE: 1997-110-17

PRIOR APPLICATION NUMBER: 60/066311

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR PILING DATE: 1997-11-21

PRIOR PILING DATE: 1998-03-11

PRIOR PILING DATE: 1998-03-12

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PRIOR PILING DATE: 1998-03-13

PRIOR PILING DATE: 1998-03-13
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                               Sequence 211, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/078939
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APPLICATION UNDER: 60/079294
FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Bottefin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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241 AVWLSWKVSGP 251
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                                                                                                           US-09-999-832A-211
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07920
PRIOR APPLICATION NUMBER: 60/080105
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PRIOR PILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-05
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PRIOR PELING DATE: 1998-05-13
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PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15 R FILING DATE: 1998-06-07

R APPLICATION NUMBER: 60/084598

R APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084643

R APPLICATION NUMBER: 60/084643 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559

ö 83.1%; Score 1337; DB 10; Length 985; 98.8%; Pred. No. 4.1e-101; ive 1; Mismatches 2; Indels 0 Best Local Similarity 98.8 Matches 248; Conservative Query Match

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LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 142 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 181 GTYMCVAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 83 Н 19 143 유 g à 원 ò 8

AVWLXWKVSGP 273 263

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Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
Goddard, Audrey
                                                                                                     Perrara, Napoleon
                         Botstein, David
Desnoyers, Luc
Eaton, Dan
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 XTYMCVATNSAGHRESRAARVSIQEPODYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GTYMCVATNSAGHRESRAARVSIOEPODYTEPVELLAVRIOLENVTLLNPDPAEGPKPRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGGMAQDSPPQILVHPQDQLFQGFQPARMSCQASGQPPTIRWLLNGQPLSMVPPDPHHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.1%; Score 1337; DB 10; Length 985; Best Local Similarity 98.8%; Pred. No. 4.1e-101; Matches 248; Conservative 1; Mismatches 2; Indels 0
                   R FILING DATE: 1998-05-05

R APPLICATION NUMBER: 60/084414

R FILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084441

R FILING DATE: 1998-05-06

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084637

R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R PILING DATE: 1998-05-13

R PILING DATE: 1998-05-15

R PILING DATE: 1998-05-15
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US-09-978-192A-211
Sequence 211, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/084366
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR APPLICATION NUMBER: 60/081229
PRIOR APPLICATION NUMBER: 60/081955
PRIOR APPLICATION NUMBER: 60/081817
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR APPLICATION NUMBER: 60/081952
PRIOR APPLICATION NUMBER: 60/081952
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-12
PRIOR APPLICATION NUMBER: 60/082569
PRIOR PILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-04-27
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R APPLICATION NUMBER: 60/081070
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071
                                                                                                                           R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
R FILING DATE: 1998-04-01
R PILING DATE: 1998-04-01
R PILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/083499
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083554
FILING DATE: 1998-04-29
                                                             FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/080334
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FILING DATE: 1998-03-31
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT APPLICATION NUMBER: US/09/978,697
REIOR PRING DATE: 1997-11-3
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
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PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-
                           Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Klov, Sophia S.
Napier, Mary A.
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APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/079923
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                                                                                                                                                                                                                                                                                             Pan, James,
Paoni, Nicholas F.
Roy, Margaret Ann
Shelron, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
Gerritsen, Mary E.
APPLICANT
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LING DATE: 1998-04-09
PLICATION NUMBER: 60/081229
LING DATE: 1998-04-09
PLICATION NUMBER: 60/081955
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ICATION NUMBER: 60/081819
NG DATE: 1998-04-15
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IG DATE: 1998-04-15
CATION NUMBER: 60/082568
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IG DATE: 1998-04-22
CATION NUMBER: 60/082796
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FILING DATE: 1998-04-30
                                                                                                                  ICATION NUMBER: 60/081071
NG DATE: 1998-04-08
                                                                                                                                                                                                                                                                                                                                                                                          GATION NUMBER: 60/081817
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NG DATE: 1998-04-15
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IG DATE: 1998-04-28
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IG DATE: 1998-04-29
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NG DATE: 1998-04-29
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ICATION NUMBER: 60/083500
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FILING DATE: 1998-05-05
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CATION NUMBER: 60/082704
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CATION NUMBER: 60/083554
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61 LPDGTLLLLQPPARGHAHDQQALSTDLGVYTCBASNRLGTAVSRGARLSVAVLREDFQIQ 120 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 240 83 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQ 203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL 143 PRDMVAVVGEQPTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE ö Length 985; Indels Score 1337; DB 10; Pred. No. 4.1e-101; 1; Mismatches 2; PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15 PILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085582 APPLICATION NUMBER: 60/085323 Query Match 83.1%; Best Local Similarity 98.8%; Matches 248; Conservative Perrara, Napoleon Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bocstein, David
APPLICANT: Desnoyers, Luc 263 AVWLXWKVSGP 273 241 AVWLSWKVSGP 251 Botstein, Davi Desnoyers, Luc APPLICANT

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Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                         Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                   Paoni, Nicholas F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
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TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
FRIOR PILING DATE: 2000-07-28
FRIOR PILING DATE: 2000-07-28
FRIOR PILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-07-17
FRIOR FILING DATE: 2000-02-17
FRIOR FILING DATE: 2000-02-17
FRIOR FILING DATE: 1999-10-18
FRIOR PILING DATE: 1999-10-18
FRIOR PAPLICATION NUMBER: UF 2000-183767
FRIOR PILING DATE: 2000-01-11
FRIOR PILING DATE: 1999-10-18
FRIOR FILING DATE: 1999-10-19
FRIOR FILING DATE: 1999-07-29
FRIOR OF SEQ ID NOS: 64
FRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1436; DB 15;
Pred. No. 2.4e-109;
1; Mismatches 3;
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Grimaldi, J. Christopher
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 98.5
Matches 269; Conservative
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Kuo, Sophia S
Napier, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapiens
US-10-059-585-22
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APPLICANT: State of the control of the contro
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: P2016P1
FILE APPLICATION NUMBER: US/09/722,329
FRIOR APPLICATION NUMBER: 09/262,109
FRIOR FILING DATE: 1999-09-05
FRIOR APPLICATION NUMBER: 60/057,663
FRIOR APPLICATION NUMBER: 60/057,663
FRIOR FILING DATE: 1997-09-05
FRIOR FILING DATE: 1997-09-05
FRIOR APPLICATION NUMBER: 60/059,667
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 60/058,974
FRIOR APPLICATION NUMBER: 60/058,973
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 60/058,973
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1998-06-22
                                      NAME/KEY: SITE
LOCATION: (203)
LOCATION: (203)
NAME/KEY: SITE
LOCATION: (267)
LOCATION: (267)
NAME/KEY: SITE
LOCATION: (287)
NAME/KEY: SITE
                                                                                                                                                                                                     ; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86
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Publication No. US20030166906A1
GENERAL INFORMATION:
ORGANISM: Homo sapiens
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                                                                                                                                                           ION: (203)
INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 1.8e-123;
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (304)
; OTHER INFORMATION: Xaa equals stop translation
US-10-411-224-86
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100.0%; Pred. No. ...
0; Mismatches
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Publication No. US20030082776A1
GENERAL INFORMATION:
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Punahashi, Shin-Ichi
                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                        INFORMATION: Xaa equals
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Ishii, Shizuko
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APPLICANT: 1809ai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 303; Conservative
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Nezu, Jun-Ichi
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver.
SEQ ID NO 86
                                                         LENGTH: 304
TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (203)
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OTHER INFO
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US-09-978-681A-211 US-09-999-829A-211

ALIGNMENTS

Sequence Sequence

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TITLE OF INVENTION:

PAPPLICANT: Rosen et al.

TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PSO16F2

CURRENT APPLICATION NUMBER: US/10/047,021

CURRENT FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: US 60/262,066

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 1999-03-04

PRIOR FILING DATE: 1999-03-04

PRIOR FILING DATE: 1999-03-04

PRIOR PRILING DATE: 1999-03-05

PRIOR PRILING DATE: 1999-03-05

PRIOR PRILING DATE: 1997-09-05

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PRIOR PRILING DATE: 1997-09-05

PRIOR PRILING DATE: 1997-09-05

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PRIOR PRILING DATE: 1997-09-12

PRIOR PILING DATE: 1999-09-00

PRIOR PILING DATE: 1999-09-0
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; Publication No. US20040002591A1
; GENERAL INFORMATION:
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SEQ ID NO 86
LENGTH: 303
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      January 30, 2004, 15:54:49; Search time 30.8756 Seconds (without alignments) 2039.494 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86,
Sequence 22,
Sequence 211,
Sequence 211,
Sequence 211,
Sequence 211,
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Sequence 211,
Sequence 211,
Sequence 211,
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                                                                                                                                                                                                                                                                                                                           US-10-047-021-86
1608
1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW FUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9E_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9E_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-047-021-86
US-10-411-224-86
US-10-059-58-22
US-09-978-295-21
US-09-978-192A-211
US-09-978-192A-211
US-09-978-189-211
US-09-978-189-211
US-09-978-189-211
US-09-978-585A-211
US-09-978-585A-211
US-09-978-585A-211
US-09-978-191A-211
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US-09-978-191A-211
US-09-978-191A-211
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US-09-978-191A-211
US-09-978-191A-211
US-09-978-191A-211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          789580 seqs, 207824079 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                          Copyright
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1602
11602
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11337
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                                                                                                                                                                                                           Run on:
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Sequence 2 Sequence 2 Sequence 2

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Query Match 14.4%; Score 232; DB 4; Length 607; Best Local Similarity 28.7%; Pred. No. 1.6e-14; Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;
                                                                                                                                                                                                                                                                                      120 VVSREAILRFGFLQE-FSKEERDPVKAHEGMGVMLPCNPPAHYPGLSYRWLLNEFPNFIP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSIQ---- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 IRWILINGQPLSMVPPDPHHILPDGTLILLLQPPARGHAHDGQALSTDLGVYTCEASNRLGT 122
                                                                                                                                                                                                                                                                                                                                                      123 AVSRGARLSVAVLREDFQIQPRDMV-AVVGEOFTLECGPPWGHPEPTVSWWKDGKPLAL- 180
                                                                                                                                                                                                 23 SAWSSALGSQTT-----FGPVFEDQPLSVL-FPEESTEE---QVLLACRARASPPAT 70
                                                                                                                                                                     3 SGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 -----EPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : | | : : | | 336 LFAPSIKARFPAETYALVGQQVTLECFAFGNPVPR------IKWRKVDG 278
; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-707-802-12
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Search completed: January 30, 2004, 15:57:51 Job time : 16.1762 secs

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linear
   TOPOLOGY:
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APPLICANT: MCCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 68 NGQPLSMVPPDPHHILPDGTILLLLQPPARGHAHDGQALST--DLGVYTCEASNRLGTAVS 125
                                                                                                                                                                                                                                                                                                                                                                       74 NSQRETIDEDE---SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                          126 RGARLSVAVLREDFQIQPRDMVAVVGEQF-----TLECGPPWGHPEPTVSWWXDGK.176
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRW-----LL 67
                                                                                                                                                                                                                                                                                            14 GPVGLFLVLARAGCLAEEPPRFIREFKDQIGVSGGVASFVCQATGDPKPRVTWNKKGKKV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 PL--ALQPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 226
                                                                                                                                                                                                                                 39;
                                                                                                                                                                                          Length 1501;
                                                                                                                                                                                                                                 82; Indels
                                                                                                                                                                                          14.8%; Score 237.5; DB 2; 30.9%; Pred. No. 1.6e-14; tive 40; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/752,307B
FILING DATE: 19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Fish & Richardson, P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08752307B
Patent No. 5952171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meiklejohn, Ph.D., Anit
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 094(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                          TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-716-679-3
                                                                                                                                                                                        Query Match
Best Local Similarity 30.99
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02110-2804
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STREET: 225 Fr
CITY: Boston
STATE: MA
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US-08-752-307B-12
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APPLICANT: MCCarthy, Sean A.
APPLICANT: MCCarthy, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                        63 IRWLLNGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AVSRGARLSVAVLREDFQIQPRDMV-AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 VVSREAILRFGFLQE-PSKEERDPVKAHEGWGVMLPCNPPAHYPGLSYRWLLNFFPNFIP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSIQ---- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SAWSSALGSQTT------FGRVFEDQPLSVL-FPEESTEE---QVLLACRARASPPAT 70
                                                                                                                                                                                                                                                                                                                                                            3 SGGDSLLGGRGSLPLLLLINGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVMLXW-KVSG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 LFAPSIKARFPAETYALVGQQVTLECFAFGNPVPR------IKWRKVDG 278
                                                                                                                                                903
                                                                                          Length 607;
                                                                                    Query Match
Best Local Similarity 28.7%; Pred. No. 1.6e-14;
Matches 84; Conservative 41; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT AFEL: DESCRIPTION
COMPATING SYSTEM: Windows95
SOFTWARE: FRANCESERS (FOR WINDOWS95
SOFTWARE: FRANCESTOR OF THE WINDOWS95
SOFTWARE: FRANCESTOR OF THE WINDOWS OF THING DATE: O'-No. 6391586-2000
CLASSIFICATION NUMBER: 08/152,307
FILING DATE: CUNKNOWN:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/752,307
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: MAILE CONTON NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09707802
Patent No. 6391586
GENERAL INFORMATION:
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INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
MOLECULE TYPE: protein US-08-752-3078-12
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US-08-447-464-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 RVTWNKKGKKVNSQRFETIEFDE----SAGAVLRIQP-----LRTPRDENVYEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 EASNRLGTAVSRGARLSVAVLRED------PQIQPRDMVAVVGEQFTLECGPPWGHPE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 VAQNSVG-EITVMAKLT--VLREDQLPSGFPNIDMGPQLKVVERTRTATMLCAAS-GNPD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTVSWWKDGKPL--ALQPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GPGMVSVVGPMG---LLVVLLVGGCAAEEPPRFIKEPKDQIGVSGRVASFVCQATGDPKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 15.3%; Score 246; DB 5; Length 191
Best Local Similarity 30.9%; Pred. No. 3.2e-15;
Matches 75; Conservative 43; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOVEL RECEPTOR-TYPE PROTEIN PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08447464

Sequence 3, Application US/08447464

Batent No. 5840842

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGN
TITLE OF INVENTION: ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York
STREET: U S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: Batchilm Release #1.0, Version #1.25
CURRENT APPLICATION NATA.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14.5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
                                                                                         NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 189:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                    TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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224 YVR 226
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US-08-447-464-3
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14 NSQRFETIDFDE----SSGAVLRIQP------LRTPRDENVYECVAQNSVG-BIT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 NGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALST--DLGVYTCEASNRLGTAVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 VHAKLT--VLRED-ÖLPPGFPNIDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GSLPLLLLINGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRW-----LL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GPVGLFLVLLARGCLAEEPPRFIREPKDQIGVSGGVASFVCQATGDPKPRVTWNKKGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 PL--ALOPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL RECEPTOR-TYPE PROTEIN PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 14.8%; Score 237.5; DB 2; Best Local Similarity 30.9%; Pred. No. 1.6e-14; Matches 72; Conservative 40; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08716679
Fatent No. 5846800
GENERAL INFORMATION:
APPLICANT: Yan, Hai
APPLICANT: Yan, Hai
TITLE OF INVENTION: PHOSPHOTYROSINE PHOS
NUMBER OF SEQUENCES: 12
CORRESPONDER PADDRESS:
CORRESPONDER PEDDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
PC-COMPUTER: IBM PC COMPALIBLE
PC-DOS/MS-DY
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 246; 30.9%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:
 APPLICATION NUMBER: US/09/158,657
                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
                                                                                                                                                                              18992DA
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                          1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Conservative
                                                                                                                                                                                                                                 732-594-4720
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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224 YVR 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 PTVSWWKDGKPL--ALQPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GPGMVSVVGPMG---LLVVLLVGGCAAEEPPRFIKEPKDQIGVSGRVASFVCQATGDPKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09158657
Patent No. 6214564
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.3%; Score 246; DB 2;
Best Local Similarity 30.9%; Pred. No. 3.2e-15;
Matches 75; Conservative 43; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: J. MARK HAND - MERCK & CO., INC.
126 E. LINCOLN AVE., P.O. BOX 2000
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERNCE/DOCKET NUMBER: 18992DA
TELEPHONE: 732-594-3905
TELEPHONE: 732-594-305
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
Floppy disk
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: RAHWAY
STATE: NEW JERSEY
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STREET: 12
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62 TIRW-----LLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALST--DLGVYTC 114
                                                                                                                                                                                                                                                           115 EASNRLGTAVSRGARLSVAVLRED-----FQIQPRDMVAVVGEQFTLECGPPWGHPE 166
                                                                                                                                                                                                                                                                                                                                                                      108 VAQNSVG-EITVHAKLT--VLREDQLPSGFPNIDMGPQLKVVERTRTATMLCAAS-GNPD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTVSWWKDGKPL---ALQPGR-HTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 GPGWVSVVGPMG---LLVVVLLVVGGCAAEEPPRFIKEPKDQIGVSGRVASFVCQATGDPKP
                                                                                                             2 GSGGDSLLGGRGSLPLLLLINGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPP
                                                         Gaps
                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application PC/TUS9410166
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A
APPLICANT: RODAN, GIDEON A
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCE: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
Score 246; DB 3; Length 1911;
Pred. No. 3.2e-15;
                                                      85; Indels
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 PQILVHPQDQLFQGPG-PARMSCRASGQPPFTIRWLLNGQPLSMVPPDPHHLLPDGTLLL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 251; DB 4; Length 630; 34.5%; Pred. No. 2.2e-16; tive 34; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                  STATE: MA
COUNTRY: US
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
Richardson, P.C.
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,326
APPLICATION NUMBER: 0595872-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-991-326-14
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/752,307
FILING DATE: 19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 XTYMCVATNSAGHRESRAARVSIQEP 228
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 GIYTCVATNILGKVEAQ-VRLEVKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08348006B Patent No. 5658756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 630 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-348-006B-5
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62 TIRW-----LLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALST--DLGVYTC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 EASNRLGTAVSRGARLSVAVLRED------FQIQPRDMVAVVGEQFTLECGPPWGHPE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GPGMVSVVGPMG---LLVVLLVGGCAAEEPPRFIKEPKDQIGVSGRVASFVCQATGDPKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGFGPARMSCRASGQPPP
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APPLICANT: RODAN, GIDEON A. APPLICANT: ROTAGES, AMEDICANT: RUTLEDGE, SU JANE; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN; TITLE OF INVENTION: TYROSINE PHOSPHATASE; NUMBER OF SEQUENCES; MADDRESS; ADDRESSE: J. MARK HAND - MERCK & CO., INC. STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 1; Length 1911; 3.2e-15;
                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 246; 30.9%; Pred. No. 3
                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
REPERENCE/DOCKET UMBER: 186
TELECOMMUNICATION: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1911 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.9%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 908-594-4720
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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ABLICANT: MCCATHY, Sean A.
APPLICANT: MCCATHY, Sean A.
Gearing, David P.
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 ------RDTQIGSS--AVYQCNASNEHGYLL---ANAFVSVL----DVPPRILAPRN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 DMVAVVGEQFT-LECGPPWGHPEPTVSWWKDGKPLALQPGRHTV-SGGSLLMARAEKSDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 PQILVHPQDQLFQGPG-PARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 PYWLDEPQN-LILAPGEDGRLVCRANGNPKPSIQWLVNGEPIEGSPPNPSREVAGDIIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR----
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15.6%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 2.2e-16;
Matches 71; Conservative 34; Mismatches 71; Indels
                                                                                                                                                                                                    COMPTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PESTENCY Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/707,802
FILING DATE: 07-00.
CLASSIFICATION: 4Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/752,307
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejöhn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/020001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-707-802-14
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515 GIYTCVATNILGKVEAQ-VRLEVKDP 539
                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09991326
Patent No. 6395872
GENERAL INFORMATION:
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TELEFAX: 617-542-8906
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                   NUMBER OF SEQUENCES: 14
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                                                                                                                                                             CITY: Boston STATE: MA
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                                                                                  APPLICANT: McCarthy, Sean A.
APPLICANT: Geating, David P.
APPLICANT: Geating, David P.
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 PYWLDEPQN-LILAPGEDGRLVCRANGNPKPSIQWLVNGEPIEGSPPNPSREVAGDTIVF 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.6%; Score 251; DB 2; Best Local Similarity 34.5%; Pred. No. 2.2e-16; Matches 71; Conservative 34; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
SOFTWARET PAPLICATION DATA:
APPLICATION NUMBER: US/08/752,307B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35,283
3R: 09404/020001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anita L.
              Sequence 14, Application US/08752307B Patent No. 5952171
GENERAL INFORMATION:
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Patent No. 6391586
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
                                                                                                                                                                                                                                                                           STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meiklejohn, Ph.D REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-752-3078-14
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                CITY: BOE
STATE: MA
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US-09-707-802-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPL----ALQP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 HASLQIAVLRDDFRVEPKDTRVAKGETALLECGPPKGIPEPTLIWIKDGVPLDDLKAMSF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 GRHT----VSGGSLIMARAEKSDEXTYMCVATNSAGHRESRAARVSIQ-EPQDYTEPVEL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GASSRVRIVDGGNLLISNVEPIDEGNYKCIAQNLVGTRESSYAKLIVQVKPYFMKEPKD- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 LPAWILLVLVVASNGLPAVRGOYOSPRIIEHPTDLVVKKNEPATLNCKVEGKPEPTIEWFK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LPLLLLLIM---GGM----AQDSPPQILVHPQDQLFQGFGPARMSCRASGQPPFTIRWLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 1395;
                                                                 APPLICANT: Tessier.—Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR PLING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/081,057
SPRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Truesier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT PILING DATE: 2000-03-31
FRIOR APPLICATION NUMBER: 60/065,544
FRIOR APPLICATION NUMBER: 60/065,544
FRIOR APPLICATION NUMBER: 60/061,057
FRIOR APPLICATION NUMBER: 60/081,057
SPRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17-07
                                                                                                                                                                                                                                                                                                                                                                                                           25.2%; Score 405; DB 3; Length 13 36.6%; Pred. No. 3.8e-31; ive 38; Mismatches 104; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 ---QVMLYGQTATFHCSVGGDPPPKVLW 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09540245A Patent No. 6270984
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.61
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
                  Goodman, Corey
                                                         Brose, Katja
                                      Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                  US-09-540-245A-15
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                                                                                                                                                                                                                                                                                                             LENGTH: 1395
                                      APPLICANT:
APPLICANT:
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Score 356.5; DB 3; Length 1297; Pred. No. 2.2e-26;

22.2%;

Query Match Best Local Similarity

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SDSGTYQCVANNWVGERVSNPARLSVFEKPKFEQEPKDMT------VDVGAAVLFDC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 QPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1QPRDMVAVVG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 TNSAGHRESRAARVS-----IQEPQDYTEPVELLAV---RIQLENVTLLNPDPAEGPK 259
                                                                                                                                                                   141
                                                                                                                                                                                                                                                                           OPROMVAVVGEOFTLECGPPWGHPEPTVSWWKDGKPLALOP-GRHTV-SGGSLLMARAEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GGD 222
                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PRIIEHPMDTTVPKNDPFTFNCQAEGNPTPTIQWFKDGRELKTDTGSHRIMLPAGGLFFL 63
                                                      27 AQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPFT--IRWLLNGQPL--SMVPPDPHHL
                                                                                         83 LPD-GTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 POILVHPODOLFOGPGPARMSCRASGOPPFIIRWLLNGQPLSMVPPDPHHLLPDGTLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
  41; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 DPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 RVTGDPQPQ----ITWK------RKNEPMPVTRAYIAKDNRGLRIER 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.5%; Score 345; DB 3; Length 1381; Best Local Similarity 33.7%; Pred. No. 3.2e-25; Matches 91; Conservative 31; Mismatches 102; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Except.
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
ITILE OF INVENTION: Modulating Robo: Ligand Interactions
ITILE OF INVENTION: MOGULATING ROBO: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
FRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
45; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 KNVVGTRESATAFLKVHVRPFLİRGPQNQİAVVGSSVVFQCRİ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLPDV--LWR-----RTASGGNMP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09540245A Patent No. 6270984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-16
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-540-245A-16
97;
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us-10-047-021-86.rai

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
             Copyright
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OM protein - protein search, using sw model

January 30, 2004, 15:53:19; Search time 15.1762 Seconds Run on:

(without alignments) 844.758 Million cell updates/sec

US-10-047-021-86 1608 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 seqs, 42310858 residues Searched:

Total number of hits satisfying chosen parameters:

328717

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued Patents AA:* 4.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	446.5	27.8	1651	3	US-09-540-245A-18	Seguence 18, Appl
2	405	25.2	1395	ო	US-09-540-245A-15	15,
٣	356.5	22.2	1297	٣	US-09-540-245A-17	17,
4	345	21.5	1381	m	US-09-540-245A-16	Sequence 16, Appl
5	251	15.6	630	~	US-08-752-307B-14	14,
9	251	15.6	630	4	US-09-707-802-14	Sequence 14, Appl
7	251	15.6	630	4	US-09-991-326-14	14,
80	246	15.3	1911	Н	US-08-348-006B-5	5,
6	246	15.3	1911	~	US-08-800-825A-5	Sequence 5, Appli
10	246	15.3	1911	m	US-09-158-657-5	'n
11	246	15.3	1911	S	PCT-US94-10166-5	'n
12	237.5	14.8	1501	~	US-08-447-464-3	m
13	237.5	14.8	1501	8	US-08-716-679-3	Sequence 3, Appli
14	232	14.4	607	~	US-08-752-307B-12	12,
15	232	14.4		4	US-09-707-802-12	12,
16	232	14.4	607	4	US-09-991-326-12	12,
17	227.5	14.1	596	~	US-08-752-307B-13	13,
18	227.5	14.1	296	4	US-09-707-802-13	13,
19	227.5	14.1	296	4	US-09-991-326-13	13,
20	206	12.8	1447	m	US-09-041-886-25	25,
21	206	12.8	1447	S	PCT-US94-05277-2	ď
22	203	12.6	615	~	US-08-752-307B-9	o,
23	203	12.6	615	4	US-09-707-802-9	o,
24	203	12.6	615	4	US-09-991-326-9	σ
25	201.5	12.5	946	'n	PCT-US95-08493-13	13
56	194.5	12.1	612	~	US-08-752-307B-11	Sequence 11, Appl
27	194.5	12.1	612	4	US-09-707-802-11	Sequence 11, Appl

18 24 2 2 1 1 1 2 2 4 5 1 8 1 1 2 2 4 2 2 1 2 1 2 1 2 1 2 1 2 1 2 1	Sequence 7, Appl1
US-09-991-326-11 US-08-506-296B-28 US-08-986-485-5 US-08-506-296B-4 US-08-506-296B-4 US-08-506-296B-1 US-08-752-307B-10 US-09-707-802-10 US-09-991-326-10 US-09-991-326-10 US-09-977-30-6 US-09-877-730-6 US-09-877-730-8	US-08-752-307B-7
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612 1268 1266 1266 1260 1101 1101 611 1203 380 984 985 1150	462
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194.5 194.5 193 193 193 186 186 186 186 186 186 186 186 175.5 175.5	175
000000000000000044444 8000100400000044444	42

ALIGNMENTS

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64 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTFTIEWYKGGERVETDKDDPRSHRMLLP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 DGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 ODSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1651;
                                                           APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Kaid, Thomas
APPLICANT: Brose, Kaid, Thomas
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-0131-3
CURRENT APPLICATION NUMBER: 06/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR PLILING DATE: 1997-11-14
PRIOR PLILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 18
LENGINE 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 YMCVATNSAGHRESRAARVSIQEPODYTEPVELLAVRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.8%; Score 446.5; DB 3; Best Local Similarity 41.7%; Pred. No. 3.7e-35; Matches 91; Conservative 31; Mismatches 87;
Sequence 18, Application US/09540245A Patent No. 6270984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: human
US-09-540-245A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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84

Gaps

238 YVCVGTNMVGERESEVAELTVLERPSFVKRPSNLAVTV 275 RESULT 2 US-09-240-245A-15 ; Sequence 15, Application US/09540245A ; Patent No. 6270984 g

MARIN WHITE THE TENNS SHALL

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64 EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP 123
                                                 85 DGTLILLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
g
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RDDFRQNPS 177	
ARNYLGEAVSHNASLEVALI	
IVHGRKSRPDEGVYVCV	
124 SGSLFFLR	
	3SLFFLRIVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEVAILRDDFRQNPS

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Search completed: January 30, 2004, 15:54:42 Job time : 40.2487 secs

²⁰⁵ YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242

²³⁸ YVCVGTNMVGERESEVAELITVLERPSFVKRPSNLAVTV 275

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DB 24; Length 753;

.3e-30

139 205

윱 ઠે ABU04090;

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in nerve guidance which heve been isolated from Drosophila sp.,
C. elegans, human and murine samples. The products of the invention can
be used to raise anti-Robo antibodies, which can be used to modulate cell
function or morphology. The Robo polynucleotides and fragments are useful
as probes and primers and for production of the Robo polypeptides. The
probes and primers are also useful in screening assays.
                                                                                                                                                                                                                                         85 SGSLFFLR-----IVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEVAILRDDFRQNPS 138
                                                                                                                                                                                                85 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
                                                                                                                                                                                                                                                                                       DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel Robo (roundabout) polypeptides, involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBO1; ROBO2; roundabout; nerve guidance; human; murine; cell function;
                                                                                                                                                    EDFPPRIVEHPSDLIVSKGEPATLNCKAEGRPTPTIEWYKGGERVETDKDDPRSHRMLLP
                                                                                                         QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHH----LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, a new immunoglobulin superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                         YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI
                                                ; Pred. No. 2.3e
31; Mismatches
                         27.8%; Score 446.5; 41.7%; Pred. No. 2.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitchell KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY08404 standard; Protein; 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     morphology; screening assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US22164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0971172
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                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kidd T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-312615/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ROBOl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1649 AA;
                                             Local Similarity
nes 91, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX08404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodman CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY08404;
                                                                                                             28
                                                                                                                                                  25
                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                              202
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Best Local
                           Query Match
                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for elicting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to processed class I or class II MRC-binding polypeptide. The polypeptides and polymulectides are particularly useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                       phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; agentic cancer; adenocarchoma; sarcoma; melanoma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                     Translational profiling; expressed protein tag; EPT; kinase;
                                                                                           YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID No 756; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                         Human expressed protein tag (EPT) #756.
                                                                                                                                                                                                                       ABU04090 standard; Protein; 753 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2001; 2001US-279495P.
21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FEB-2002; 2002US-358985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2002; 2002WO-US09671
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         753 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200278524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                           29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicz RM,
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7
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                                                                      Gaps
Similarity 41.7%; Pred. No. 6.3e-30; Length 1649; Similarity 41.7%; Pred. No. 6.3e-30; Similarity 41.7%; Mismatches 87; Indels 9;
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85 DGTILLLOPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 DMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLIMARAEKSDEXT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 QDSPPQILVHPQDQLFQGPGPARMSCRASGQPPFTIRWLLNGQPLSMVPPDPHH---LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a novel human protein designated TB5, and also referred to as FMHB-6D4 and FMHB-SD4. TB5 CDNA (see AAV69278) was identified in a human foetal brain CDNA library using a screen designed to identify genes encoding proteins having a functional signal sequence. TB5 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological
                                                                                                 43..101
/note= "has homology to a Ig superfamily domain"
                                                                                                                                                            "has homology to a Ig superfamily domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
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'note= "has homology to a fibronectin type III
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                                                                                                                                                                                                                                                                                                                                                                 'note= "cytokine receptor homology N-terminal
                                                           to a fibronectin type
                                                                                                                                                                                                    "has homology to a Ig superfamily
                                                                                                                                                                                                                                          "has homology to a Ig superfamily
                                                                                                                                                                                                                                                                                     superfamily
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41.7%; Pred. No. 2.3e-30;
iive 31; Mismatches 87;
                                                                                                                                                                                                                                                       433..491
/note= "has homology to a Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                         'note= "has homology
                                                                                                                                                                                                                                                                                                              /note= "RGD motif"
:16..600
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                   domain"
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                                                                                                                                                                                                                       .394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCarthy SA;
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                                      638..727
                                                                                                                                                                                 .298
                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                            note=
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N-PSDB; AAV69278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            753 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                          The present sequence representing human TANGO 330 form 1 is isolated from cDNA 10ne jthAa060g22 from a human adrenal gland cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins which also includes TANGO 315 (A 4 novel human transmembrane proteins which also includes TANGO 315 (AAU00498-AAU00499). TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins are madulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acid molecules and containing the TANGO nucleic acids are also described. Diagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids are also described. Containing the TANGO nucleic acids are used diagnostically to mucleic acids and to identify compounds that bind to or modulate activity of the TANGO proteins. Anti-TANGO attibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids and proteins may be used to diagnose, treat and monitor disorders of the and proteins may be used to cliagnose, treat and monitor disorders of the can also be used to treat cell proliferative disorders (e.g. cancer), and neurological disorders e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 QFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCVATNS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLSWKVSG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 PPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEXTYMCVATNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabs
                                                                       Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHMB-6D4; FMHV-SD4; human; neurological disorder; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 934;
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Pred. No. 9.4e-75;
0; Mismatches 2;
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/label= Sig_peptide
21..73 Mat_protein
525..610
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                                                                                                                                                        Claim 9; Fig 13; 261pp; English
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Best Local Similarity 98.9
Matches 179; Conservative
                WPI; 2001-235372/24.
N-PSDB; AAS01694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 AA;
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/label= Transmembrane_domain
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                                                                                                                                       .474
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53..555
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                                              Domain
                                                                                       Human; TANGO 315; clone jthAa060g22; TANGO 330; TANGO 437; TANGO 480; cellular process regulator; gene therapy; adrenal gland; cancer; Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia; cell proliferative disorder; neurological disorder; Alzheimer's disease.
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note= "Protein kinase C phosphorylation site"
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te= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                         3
/note= "Alternatively this residue is Val due
species variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Protein kinase C phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                due
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                                                                                                                                                                                                                                                                                                        "Alternatively this residue is Ser due species variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is Lys due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                             is Asp
                                                                                                                                                                                                                                                             "Alternatively this residue species variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Alternatively this residue species variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .176
:e= "Asn is N-glycosylated"
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'note= "N-myristylation site"
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                                                                                                                                                                                                                   1..393
/label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8..136
label= Ig-like_domain
                                                                                                                                                                                                Location/Qualifiers
                                                            Human TANGO 330 form 1 protein.
                               (first entry)
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/note=
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                                                                                                                                                                     Homo sapiens
                              18-JUL-2001
AAU00500;
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.559
:e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                              .703
:e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .898
te= "Protein kinase C phosphorylation site"
                                                                         "Casein kinase II phosphorylation site"
                                                                                                               "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                          .635
.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.714
note= "Casein kinase II phosphorylation 21..724
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129..932
/mnte= "Casein kinase II phosphorylation
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.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                        "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                          "Protein kinase C phosphorylation
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                                                                                                                                                                                                                                                                                                                              .606
:e= "N-myristylation site"
                                                                                                                                                                                          "N-myristylation site"
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"N-myristylation site"
                                    label= Cytoplasmic_domain
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(IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                               06-NOV-2000; 2000US-245566P.
                                                                                                                                      06-NOV-2001; 2001WO-GB04906
                                                                                                                                                                                                                                                                                                     Bicknell R, Huminiecki L;
                                                                                                                                                                                                                                                                                                                                                2002-508120/54.
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK87138
                                           WO200236771-A2.
                                                                                        10-MAY-2002
  Mus sp.
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<del>g</del>
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                                                                                                                                                                                                                   The present sequence representing human TANGO 330 form 2 is isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA isolated from cDNA clone Jthxe181e12 from a human astrocyte cDNA library. TANGO 330 is 1 of 4 movel human transmembrane proteins which also includes TANGO 315 (AAU00499-AAU00499), TANGO 437 (AAU00502) cand TANGO 480 (AAU00503). The nucleic acids encoding these proteins care useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antiense nucleic acid molecules and companion of containing the TANGO nucleic acids are also described. Condesic acids and to identify compounds that bind to or modulate activity contein levels in tissue as a clinical testing procedure. TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 330 shows homology to human Roundabout. TANGO 330 uncleic acids and proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat cell proliferative disorders (e.g. cancer), can also be used to treat e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TYMCVAINSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 RDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 PDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 RDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 GGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 PDGTLLLLLOPPARGHAHDGOALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQP
                                                                                      Isolated secreted proteins and their encoding nucleic acids are used for diagnosis and treatment of e.g. bacterial and viral infections, autoimmune diseases and inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour neovasculature; cardiac disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 1332; DB 22; Length 480; 98.8%; Pred. No. 4.1e-108; ive 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endometriosis; hypoxic condition; angiogenesis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU99420 standard; Protein; 1015 AA.
                                                                                                                                                                               Claim 9; Fig 14; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.8
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 VWLXWKVSGP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 VWLSWKVSGP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ECSM4 protein #1.
                     2001-235372/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 AA;
                                        N-PSDB; AAS01695
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The present invention relates to endothelial cell-specific molecule 4 (BCSM4), and the polynucleotide sequences encoding it. The BCSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, the manufacture of diagnosit or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac disease, or endometricals by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometricals or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful in for modulating angiogenesis in an individual. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 PTIRWILINGQPLSMATPDLHYLLPDGTLLLHRPSVQGRPQDDQNILSAILGVYTCEASNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LGTAVSRGARLSVAVLQEDFQIQPRDTVAVVGESLVLECGPPWGYPKPSVSWWKDGKPLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQ-ALSTDLGVYTCEASNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIOEPODYTEPVELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Score 1112.5; DB 23; Length 1015; 77.4%; Pred. No. 1.7e-88; tive 20; Mismatches 41; Indels 1; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 VRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGP
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                                                                                                                                                            Disclosure; Fig 13; 248pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU00500 standard; Protein; 934 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represents a mouse ECSM4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.4 Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1015 AA;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for linking bioactive molecules activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and causes bioactive molecule maybe a toxin, radiolabel or antibody, and causes appropriate molecule maybe a toxin, radiolabel or antibody, and causes appropriate insufficiency, nervous system disorders, kidney disorders, cardiac insufficiency, nervous system disorders, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for sequences an analysis of individuals with genetic disorders, and in gene therapy.

**Manish of individuals with genetic disorders, and in gene therapy.

**Manish of individuals with human PRO polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TANGO 315; clone Jthxel8le12; TANGO 330; TANGO 437; TANGO 480; cellular process regulator; gene therapy; astrocyte; cancer; Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia; cell proliferative disorder; neurological disorder; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGGMAQDSPPQILVHPQDQLFQFPRARSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html.
encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1337; DB 24;
Pred. No. 3.7e-108;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                      Claim 12; Fig 77; 459pp; English.
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Best Local Similarity 98.8%;
Matches 248; Conservative
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/note= "cAMP and cGMP dependent protein kinase
phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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note= "Tyrosine kinase phosphorylation site"
                                                                                                    21..480
/label= Mature_TANGO_330_form_2_protein
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ce= "Asn is N-glycosylated"
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:e= "N-myristylation site"
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                                                                    21..480
/label= Extracellular_domain
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                   /label= Signal peptide
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156..461
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Peptide
                                                                                                    Protein
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Novel secreted and transmembrane polypeptides and polynucleotides
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09-JUL-2001;
17-OCT-1997;
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05-JUN-2001;
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20-MAR-1998;
20-MAR-1998;
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12-MAR-1998
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27-MAR-1998
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17-MAR-1998
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14-MAY-1999
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61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQ1Q 120
1 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL 60
                                                          121 PRDMVAVVGEQFTLECGPFWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDE
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                                                                                  XTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP
                                                                                                                                                                                                                                           immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia; cardiac insufficiency; nervous system disorder; kidney disorder; bone disorder; cartilage disorder; arthritis; tumour; wound healing; genetic disorder; cytostatic; antidabetic; antiinflammatory; cardiant.
                                                                                                                                                                                                                                         Human; PRO polypeptide; secreted and transmembrane protein;
                                                                                                                                                                        ABU61102 standard; Protein; 985 AA
                                                                                                                                                                                                                                                                                                                                                                                98WO-US24855.
99WO-US0106.
99WO-US05028.
99WO-US10733.
99WO-US1252.
99WO-US2851.
99WO-US28551.
99WO-US28551.
99WO-US28551.
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2000WO-US00376
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2000WO-US04341
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2000WO-US15264
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18-FEB-2000;
24-FEB-2000;
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Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Baton D, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
                                               2001WO-US09552
2001WO-US109552
2001WO-US117092
2001WO-US117090
2001WO-US117066
2001WO-US117066
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99US-018731
99US-0218217
99US-03180137
2000WO-US32678.
2000WO-US34956.
2001WO-US06520.
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2000US-0723749.
2000US-0747259.
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2001US-0874503.
2001US-0882636.
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2001US-0918585
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                                                   22-MAR-2001;
25-MAY-2001;
01-JUN-2001;
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27-NOV-2000;
20-DEC-2000;
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(first entry)

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Human, secreted protein; transmembrane protein, PRO; EST; cytostatic; expressed sequence tag; detection; cancer.
                                           Human PRO860 (UNQ421) protein sequence SEQ ID NO:211
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05-JAN-2000;
06-JAN-2000;
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Ferrara N, F:
Goddard A, G
Kljavin IJ, 1
                                                                                                   Homo sapiens
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                      08-FEB-2001
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AAB44272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                         The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to AAY41774 represent polymucleotide and polymeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHL
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                                                                                                                                                                                                                                                                        New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.1%; Score 1337; DB 20; Length 985; 98.8%; Pred. No. 3.7e-108; ive 1; Mismatches 2; Indels 0;
                                                                                                                                                                                                                  Chen J;
                                                                                                                                                                                                                   Yuan J, Baker KP,
                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 77; 530pp; English.
                                                                                                                                                                                                                   Wood WI, Goddard A, Gurney A,
         98US-0085582.
98US-0085689.
98US-008569.
98US-0085700.
98US-0086023.
98US-0086392.
98US-0086436.
98US-0086436.
98US-0086436.
98US-0087098.
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Matches 248; Conservative
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                                                                                                                                                                                                                                       WPI; 1999-551358/46.
N-PSDB; AAZ34069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                985 AA;
                     15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
18-MAY-1998;
22-MAY-1998;
                                                                                                                                                                      11-SEP-1998
                                                                                                                         28-MAY-1998
                                                                                                                                               28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
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99WO-US05028. 99US-0123957. 99US-0126773. 99US-0130232.

99US-0134287. 99US-0141037. 99US-0145698. 99US-0162506.

99WO-US28313 99WO-US28565 99WO-US30095 99WO-US31243 99WO-US31274 2000WO-US00219

99WO-US28551

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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78877 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 MGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHL
                                                                                                                                                                                                                                                                                                                                                 Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate
KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen MB;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
RA, Tumas D, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 77; 636pp; English.
       AJ, Baker KP,
Filvaroff E,
Godowski PJ,
Kuo SS, Nag,
                                                                                                                                                                Stewart TA,
                                                                                                                                                                                                                                   WPI; 2000-611443/58.
                                                                                                                                                                                                                                                                                                                                                                                            to target bioactive cellular activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 985 AA;
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AAB44272 standard; Protein; 985 AA

RESULT 8 AAB44272

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9805 - 0077649
9805 - 0077764
9805 - 0077764
9805 - 00777791
9805 - 0078910
9805 - 0079886
9805 - 0079891
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12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-MAR-1998;
20-MAR-1998;
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25-MAR-1998;
26-MAR-1998;
27-MAR-1998;
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27-MAR-1998;
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15-MAY-1998;
15-MAY-1998;
                      11-MAR-1998
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07-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                        The present sequence represents a human protein kinase/protein phosphatase. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used target molecules fir drug development.
                                  Yamamoto J;
F, Funahashi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PTIRWILINGQPLSMVPPDPHHILPDGTLILLQPPARGHAHDGQALSTDLGVYTCEASNRL
                                                                                                                   New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                         Score 1436; DB 22; Length 792;
Pred. No. 6e-117;
1; Mismatches 3; Indels 0:
                                  Saito K, Yam
, Otsuki T,
                     feogai T, Nishikawa T, Hayashi K, St
Sugiyama T, Wakamatsu A, Nagai K,
Nezu J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIQLENVILLNPDPAEGPKPRPAVMLSWKVSGP 273
                                                                                                                                                                   Claim 2; Page 175-180; 336pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO860 protein sequence.
                                                                                                                                                                                                                                                                                                                              89.3%;
98.5%;
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.5
Matches 269; Conservative
          (HELI-) HELIX RES INST
                                                                                 WPI; 2001-564736/63.
N-PSDB; AAH78073.
                                                                                                                                                                                                                                                                                                      792 AA;
                                 Isogai T,
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                                            Ishii S,
Senoo C,
                                                                                                                                                                                                                                                                                                        Sequence
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Ishii S
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11-JAN-2000;
17-FEB-2000;
02-MAY-2000;
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                                                                                                                                                                                       GTAVSRGARLSVAVLREDPQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                 1 MGSGGDSLLGGGRGSLPLLLLLIMGGMAQDSPPQ1LVHPQDQLFQGFGPARMSCQASGQPP
                                                                                        1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP
                                                                                                                              PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL
                                                                                                                                                                                                           QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polymucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy
for modulating angiogenesis in an individual. The present sequence represents human ECSM4 protein.
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                                                   Length 1104;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K, Y. Otsuki T;
                                                  DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 18085; 2537pp + CD ROM; English.
                                                 Score 1444; DB 23
Pred. No. 1.8e-117
1; Mismatches 2
                                                                                                                                                                                                                                                   RIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGP 273
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, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:18085.
                                                                                                                                                                                                                                                                                                                     AAB95515 standard; Protein; 792
                                                 89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0248036
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                          Local Similarity 98.9
Les 270; Conservative
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                               1104 AA;
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                               Sequence
                                                                                                                              61
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to the complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide which comprises a 3'-end sequence complementary to a polymucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1 east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the bespecification. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the chefull-length cDNAs. The primers also useful for synthesis encoded by the full-length cDNAs. The primers also wobtaining of the full-length cDNAs as assily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18732 represent human cDNA sequences; AAB92846 to AAH13632 represent human amino acid sequences; and AAH13622 to AAH13632 tepresent invention.

c the present invention.
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Pred. No. 6e-117;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RIQLENVTLLNPDPAEGPKPRPAVMLSWKVSGP.273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.3%;
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2000US-0183322.
2000JP-0183767.
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Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200109345-A1.
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PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL

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The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                          Human, antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                 QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV
QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV
                                                          RIQLENVILLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
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بنا
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asundi V, Zhar
T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 578; 509pp; English.
                                                                                                                                                                                                                                ABB97310 standard; Protein; 1007 AA.
                                                                                                                                                                                                                                                                                                                              Novel human protein SEQ ID NO: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2001; 2001WO-US26015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Zhou P,
Yang Y, Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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NTG 303
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                                                                                                                      NTG 303
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The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnosite or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculature, cardiac disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful
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61 PTIRWELNGQPESNVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL
                                                                               GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL
                                                                                                                                                              181 QPGRHTVSGGSLIMARAEKSDEGTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV
                                                                                                                                     181 QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV
                                                          GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, endothelial cell-specific molecule 4, ECSM4; neovasculature, imaging vascular endothelium; proliferative disease; cancer; psoriasis, diabetic retinopathy, atherosciencosis, menorrhagia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic;
                                                                                                                                                                                                                    241 RIQLENVILLNPDPAEGPKPRPAVWLXWKVSGP 273
                                                                                                                                                                                                                                             241 RIQLENVTLLNPDPAEGPKPRPAVMLSWKVSGP 273
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                                                                                                                                                                                                                                                                                                                                                             AAU99419 standard; Protein; 1104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; ABK87137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ECSM4
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Indels

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1; Mismatches

Matches 270; Conservative

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Local Similarity

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MGSGGDSLLGGRGSLPLLLLLINGGMAQDSPPQILVHPQDQLPQFGFPARMSCQASGQPP

1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP

%XCCCCCCCCCCCX%XXZCCCCCX

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arthritic disorder; asthma; immunodeficiency disease; AIDS;
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                                                                          Key .
Peptide
                                                                                                                     Protein
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                                                                                                                                                         The invention relates to novel genes (AB092553-AB092607) and proteins (ABP62013-ABP62153) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                        New polynuclectides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGSGGDSLLGGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIIRMILINGQPLSMVPPDPHHLLPDGTLLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         99.6%; Score 1602; DB 23; Length 303; 100.0%; Pred. No. 5.3e-132; ive 0; Mismatches 0; Indels 0.
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                                                                                                                                   Claim 11; Fig 1; 785pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 303; Conservative
               2002-599716/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              303 AA;
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                              N-PSDB; ABQ92573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       their corresponding polynucleotides are useful for preventing, treating or ameliorating medical conditions, e.g. by procein or gene treating or ameliorating medical conditions, e.g. by procein or gene therapy. Pathological conditions can also be diagnosed by determining the presence of mutations in the new polynucleotides. Specific uses are presence of mutations in the new polynucleotides. Specific uses are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, seletal disorders, shindisorders, and disorders, and included injuries, allery, hematopoietic disorders, seletal disorders, neurological disorders, arthritic disorders, asthma, immunodeficiency diseases, arthritic rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PTIRWILNGQPLSMVPFDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders, tumours, immune disorders, inflammation or haematological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Pred. No. 5.3e-132;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore PA,
                                                                                                                                                                                                         /note= "secreted protein"
                                                                                                                                  1..27
/note= "signal peptide"
28..303
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                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lafleur DW,
Shi Y;
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97US-0057663.
97US-0057669.
97US-0058666.
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transplant rejection; ss.
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Ruben SM,
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Matches 303; Conserv
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                                                      Homo sapiens.
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January 30, 2004, 15:44:59 ; Search time 39.2487 Seconds (without alignments) 1225.369 Million cell updates/sec
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1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985...
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985...
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.: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
:: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.
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/SIDS1/gcgdata/geneseg/genesegp-embl/AA1995
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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117:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human secreted pro	Amino acid sequenc	Novel human protei	Human ECSM4 protei	Human protein sequ	Amino acid sequenc	Human PRO860 prote	Human PRO860 (UNQ4	Human PRO860 polyp
SUMMARIES		ABP62033	AAY12934	BB97310	AU99419	AB95515	AG67430	AY41716	AB44272	ABU61102
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de	Query Match Length DB 1	9.66	99.6	89.8	89.8	89.3	89.3	83.1	83.1	83.1
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Human TANGO 330 fo Mouse ECSM4 protei	TANG	T85 pr	Human expressed pr	Human ROBO1 protei	Human expressed pr	_	Human expressed pr		Human expressed pr	Human expressed pr	Drosophila Robo 1	Drosophila sp. ROB	Drosophila melanog	Human neurotransmi	Human neurotransmi	C. elegans Robo po					Drosophila melanog	Melanoma associate	Human p53 target m	Angiogenesis-assoc	Human peroxidasin	Human secreted pro	Human protein SEQ	Human protein SEQ	Human cytoskeleton	Human cytoskeleton	NOVX related prote	Drosophila melanog	Human protein NOV9	Human immunoglobul
AAU00501 AAU99420	AAU00500	AAW83927	ABU04090	AAY08404	ABU04091	AAY13566	ABU04089	ABU04092	ABU04093	ABU04094	AAY13563	AAY08401	ABB68257	AA019185	AA019179	AAY13565	AAY08403	AAY08402	AAY13564	ABB61552	ABB61502	AAW81030	AAY70469	ABU03498	ABB11587	AA021660	AAM78714	AAM78715	AAE32108	AAE32109	ABJ19347	ABB57771	ABU07377	AAE14781
22	22	20	24	20	24	20	24	24	24	24	20	20	22	23	23	70	20	20	20	22	22	50	21	24	22	23	22	22	24	24	24	22	24	23
480	93	753	753	1649	1649	1651	1651	1651	1651	1651	1395	1395	1395	1515	1422	1297	1297	1380	1381	823	882	1496	1496	1496	1498	1463	937	952	1267	1359	1370	1527	3931	793
82.8	59.4	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	25.2	25.2	25.2	25.2	24.7	. 22.2	22.2	21.5	21.5	20.1	19.1	16.6	16.6	16.6	16.6	16.5	16.2	16.2	16.2	16.2	16.2	16.1	15.8	15.8
1332	955	446.5	446.5		446.5		446.5	446.5	446.5	446.5	405	405	405	404.5	396.5	356.5	356.5	345	345	323	307	267.5	267.5	267.5	267.5	265.5	260.5	260.5	260.5	260.5	260.5	259	54.	ë.
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	. 36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ABP62033 standard; Protein; 303 AA

ABP62033;

immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidlabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine. Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; Rosen CA, Olsen H; Shi Y, secreted protein SEQ ID NO 86. LaFleur DW, (HUMA-) HUMAN GENOME SCI INC. 18-JAN-2001; 2001US-262066P. 17-JAN-2002; 2002WO-US01109. (first entry) Moore PA, Ruben SM, Ebner R, Brewer LA; WO200257420-A2. Homo sapiens. 12-NOV-2002 25-JUL-2002 Human

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84 VYICEASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVV---GEOFTLECGPPWGHPEP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 SYOCVATNARGTVVSREASLRFGFLOE-FSAEERDPVKITEGWGVMFT--CSPPPHYPAL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 MSCRASGQPPPTIRWLLNGQPLSNVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLG 83
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 TVSWWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE---
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Pfam; PF00047; ig; 6.

SMART; SM0060; FN3; 4.

SMART; SM00408; IGC2; 5.

PROSITE; PSC6035; IG_LKE; 6.

Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor; Cell adhesion; Repeat; 3D-structure.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
H-LINKED (GLCNAC. ) (N-LINKED (GLCNAC. ) (N-LI
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les 86;
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
                                                                                                                                                                                                                                                                                                                                                  OR 25 (POTENTIAL).
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Best Local Similarity 30.7%; Pred. No. 2.9e-
Matches 70; Conservative 31; Mismatches
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               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                   CONTACTIN
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                                                                                                                 InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                     EMBL; X63101; CAA44815.1; -. PIR; S22383; S22383.
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                                                                                                DB; 1CS6; 19-MAY-00
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Q13308; Q13417;
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PTK7 OR CCK4.
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                                                                                                                                                                                            63 LLQPPARGHAHDGQALSTDLGVYTCEAS-NRLGTAVSRGARLSVA------- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         :| :|
165 AGNGAILNCEVNADLVPFVRWEQNRQPLLLDDRVIKLPSGMLVISNATEGDGGLYRCVVE 224
                                                                                                                                                                                                                                                                                                                                                                                                                       -- FOIOPRDMVAVVGEOFTLECGPPWGHPEPTVSWW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                          225 SGGPPKYSDEVELKVLPDPEVISDLVFLKQPSPLVRVIGQDVVLPCVAS-GLPTPTIKWM 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDGKPLALQPGRHTV--SGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQD 203
                                                                                                                                                                             62
                                                                                                                                                      3 SPPQILVHPQDQLFQCPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 214.5; DB 1; Length 1461;
22.7%; Pred. No. 3.6e-09;
tive 39; Mismatches 117; Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92114898; PubMed=1311675;
Zuellig R.A., Rader C., Schroeder A., Kalousek M.B.,
Zuellig R.A., Rader C., Schroeder A., Kalousek M.B.,
Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;
"The axonally secreted cell adhesion molecule, axonin-1. Primary
structure, immunoglobulin-like and fibronectin-type-III-like domains
and 91ycosy1-phosphatidylinosicol anchorage.";
Function: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM II (G4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 6 immunoglobulin-like C2-type domains. SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 LKQPTNIYA----HESMDIVFECEVTG-KPTPTV--KWVKNGDMVIPS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 YTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPN 251
                                                                                                                                                                                                                                                                                                                                   -----VLRED-----
/FTId=VSP 002593.
168 168 G -> N (IN REF. 2).
1461 Aa; 159958 MW; 7AAE897E69635A21 CRC64;
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(Rel. 24, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: The N-terminus is blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contactin 2 precursor (Axonin-1)
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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01-DEC-1992
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                   CONFLICT
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